



```
Db 61 VIFSTRGRLEYANNVSRGTIERKKACSDAVNPPSVTEANTQYQQEASKLRRQIRDIQ 120
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QY 121 NSNRHIVGESLGLNFKELKLEGRLEKISRVRSKKNELLVAETIYMOKREMELOHNNM 180
|||
Db 121 NSNRHIVGESLGLNFKELKLEGRLEKISRVRSKKNELLVAETIYMOKREMELOHNNM 180
|||
QY 181 YLRAKIATAGARLNPDQOESSVIQGTIVYESGVSSHDSQSHYNNRNYIPVNLLEPNQOQFSGQ 240
|||
Db 181 YLRAKIATAGARLNPDQOESSVIQGTIVYESGVSSHDSQSHYNNRNYIPVNLLEPNQOQFSGQ 240
|||
QY 241 DQPPLQLV 248
|||
Db 241 DQPPLQLV 248
|||

RESULT 2
US-09-349-677-6
; Sequence 6, Application US/09349677
; Patent No. 6288305
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Ferrandiz, Cristina
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/349,677
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/067,800
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-349-677-6

Query Match 100.0%; Score 1263; DB 4; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.9e-119;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEEGGSSHDAESSKLGKRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVAL 60
|||
Db 1 MEEGGSSHDAESSKLGKRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVAL 60
|||
QY 61 VIFSTRGRLEYANNVSRGTIERKKACSDAVNPPSVTEANTQYQQEASKLRRQIRDIQ 120
|||
Db 61 VIFSTRGRLEYANNVSRGTIERKKACSDAVNPPSVTEANTQYQQEASKLRRQIRDIQ 120
|||
QY 121 NSNRHIVGESLGLNFKELKLEGRLEKISRVRSKKNELLVAETIYMOKREMELOHNNM 180
|||
Db 121 NSNRHIVGESLGLNFKELKLEGRLEKISRVRSKKNELLVAETIYMOKREMELOHNNM 180
|||
QY 181 YLRAKIATAGARLNPDQOESSVIQGTIVYESGVSSHDSQSHYNNRNYIPVNLLEPNQOQFSGQ 240
|||
Db 181 YLRAKIATAGARLNPDQOESSVIQGTIVYESGVSSHDSQSHYNNRNYIPVNLLEPNQOQFSGQ 240
|||
QY 241 DQPPLQLV 248
|||
Db 241 DQPPLQLV 248
|||
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Db 121 NSNRHIVGESLGLNFKELKLEGRLEKISRVRSKKNELLVAETIYMOKREMELOHNNM 180
|||
QY 181 YLRAKIATAGARLNPDQOESSVIQGTIVYESGVSSHDSQSHYNNRNYIPVNLLEPNQOQFSGQ 240
|||
Db 181 YLRAKIATAGARLNPDQOESSVIQGTIVYESGVSSHDSQSHYNNRNYIPVNLLEPNQOQFSGQ 240
|||
QY 241 DQPPLQLV 248
|||
Db 241 DQPPLQLV 248
|||

RESULT 3
US-09-067-800-8
; Sequence 8, Application US/09067800
; Patent No. 6198024
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Ferrandiz, Cristina
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/067,800
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-067-800-8

Query Match 83.1%; Score 1050; DB 4; Length 246;
Best Local Similarity 85.5%; Pred. No. 5.7e-98;
Matches 212; Conservative 12; Mismatches 22; Indels 2; Gaps 1;

QY 1 MEEGGSSHDAESSKLGKRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVAL 60
|||
Db 1 MEEGGASNEVAESSKLGKRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVAL 60
|||
QY 61 VIFSTRGRLEYANNVSRGTIERKKACSDAVNPPSVTEANTQYQQEASKLRRQIRDIQ 120
|||
Db 61 VIFSTRGRLEYANNVSRGTIERKKACSDAVNPPSVTEANTQYQQEASKLRRQIRDIQ 120
|||
QY 121 NSNRHIVGESLGLNFKELKLEGRLEKISRVRSKKNELLVAETIYMOKREMELOHNNM 180
|||
Db 121 NENRHILGESLGLNFKELKLEGRLEKISRVRSKKNELLVAETIYMOKREIELONDNM 180
|||
QY 181 YLRAKIATAGARLNPDQOESSVIQGTIVYESGVSSHDSQSHYNNRNYIPVNLLEPNQOQFSGQ 240
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Db 181 YLRSKITE--RTGLQQOESSVIHQGTIVYESGVTSSSHOSGOYNNRNYTAVNLLLEPNQNSNQ 238
|||
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QY 241 DQPLQLV 248  
Db 239 DQPLQLV 246

RESULT 4

US-09-349-677-8  
; Sequence 8, Application US/09349677  
; Patent No. 628305  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin F.  
; APPLICANT: Ferrandiz, Cristina  
; TITLE OF INVENTION: Seed Plants Characterized by Delayed  
; TITLE OF INVENTION: Seed Dispersal  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/349,677  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/067,800  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UD 2948  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 246 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-349-677-8

Query Match 83.1%; Score 1050; DB 4; Length 246;  
Best Local Similarity 85.5%; Pred. No. 5.7e-98;  
Matches 212; Conservative 12; Mismatches 22; Indels 2; Gaps 1;

QY 1 MEEGSSHDAESSKKLGRGKIEIKRIENTTNRQVTFCKRRNGLLKAYELSVLCDAEVAL 60  
Db 1 MEGGASNEVAESSKKIGRGKIEIKRIENTTNRQVTFCKRRNGLLKAYELSVLCDAEVAL 60  
QY 61 VIFSTRGRLEYANNVSGRTIERYKKACSDAVNPPSVTEANTQYYQOEASKLRRQIRDIQ 120  
Db 61 VIFSTRGRLEYANNVSGRTIERYKKACSDAVNPPSVTEANTQYYQOEASKLRRQIRDIQ 120  
QY 121 NSNRHIVGESLGNFKELKNLEGRLEKISRVRSKKNELLVAEIEYMQKREMELOHNNM 180  
Db 121 NLNRHILGESLGNFKELKNLESRLKISRVRSKKHEMLVAEIEYMQKREIELQNDNM 180  
QY 181 YLRAKIETAGRLNPQOQESSVIGTIVYESGVSSHDSQHYNNRNYIPVNLLEPNQOFSQ 240  
Db 181 YLRSKITE--RTGLQOQESSVHQGTIVYESGVTSQSGQYNNRNYIAVNILLEPNQSSNQ 238  
QY 241 DQPLQLV 248  
Db 239 DQPLQLV 246

RESULT 5

US-08-460-512-7  
; Sequence 7, Application US/08460512  
; Patent No. 5744693  
; GENERAL INFORMATION:  
; APPLICANT: MEYEROWITZ, Elliot M.  
; APPLICANT: YANOFSKY, Martin F.  
; APPLICANT: MA, Hong  
; TITLE OF INVENTION: PLANTS HAVING ALTERED FLORAL DEVELOPMENT  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Richard F. Trecartin  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/460,512  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/293,278  
; FILING DATE:  
; APPLICATION NUMBER: US/07/956,694  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Trecartin, Richard F.  
; REGISTRATION NUMBER: 31,801  
; REFERENCE/DOCKET NUMBER: A-57322/RFT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 248 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-460-512-7

Query Match 63.9%; Score 806.5; DB 1; Length 248;  
Best Local Similarity 65.6%; Pred. No. 2e-73;  
Matches 160; Conservative 36; Mismatches 43; Indels 5; Gaps 2;

QY 7 SHDAESSKKLGRGKIEIKRIENTTNRQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTR 66  
Db 8 TREISPPQRKILGRGKIEIKRIENTTNRQVTFCKRRNGLLKAYELSVLCDAEVALVIFSSR 67  
QY 67 GRLEYANNVSGRTIERYKKACSDAVNPPSVTEANTQYYQOEASKLRRQIRDIQNSNRHI 126  
Db 68 GRLEYANNVSKATIERIYKKACSDSSNTSGISEANAQYYQOEASKLRAQIGNLQNNRNM 127  
QY 127 VGESLGSNFKELKNLEGRLEKISRVRSKKNELLVAEIEYMQKREMELOHNNMILRAKI 186  
Db 128 LGESLAALSRLDLKNLEQKIEKISRSKNELLFAEIEYMQKREIDLHNNNQYLRAKI 187  
QY 187 AEGARLNPQOQES--SVIOGTIVYESGVSSHDSQHYNNRNYIPVNLLEPNQOFSQDQPP 244  
Db 188 AETERAQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQO 244  
QY 245 LQLV 248  
Db 245 LQLV 248

RESULT 6

```

US-09-433-579-2
; Sequence 2, Application US/09433579
; Patent No. 6444877
; GENERAL INFORMATION:
; APPLICANT: Rottmann, William H.
; TITLE OF INVENTION: LSAG Gene
; FILE REFERENCE: LSAG Gene
; CURRENT APPLICATION NUMBER: US/09/
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 226
; TYPE: prt
; ORGANISM: Liquidambar styraciflua
US-09-433-579-2

```

|    | Query Match           | 61.0%;                                                         | Score 770.5;       | DB 4;     | Length 226; |
|----|-----------------------|----------------------------------------------------------------|--------------------|-----------|-------------|
|    | Best Local Similarity | 68.2%;                                                         | Pred. No. 7.4e-70; |           |             |
|    | Matches 159;          | Conservative 29;                                               | Mismatches 38;     | Indels 7; | Gaps 2;     |
| Qy | 16                    | LGRGKIEIKRIENTTNROVTECKRRRNGLLKKAYELSVLCDAEVALVIFSTRGRLEYEYANN | 75                 |           |             |
| Db | 1                     | MGRGKIEIKRIENTTNROVTECKRRRNGLLKKAYELSVLCDAEVALVIFSTRGRLEYEYANN | 60                 |           |             |
| Qy | 76                    | SVRGTIERYKKACSDAVNPPSPVTEANTQYQOEAKLRRQIRDIQNSNRHIVGESLSGLN    | 135                |           |             |
| Db | 61                    | SVKATIERYKKASVDSSNTGVSSEANAQFYQOEAGKLNRQIRNMQNTNRTMLGESLSLS    | 120                |           |             |
| Qy | 136                   | FKELKNLEGRLEKGISRVRKKNELLVAEIEYMQKREMLQHNMMYLRAKIAEAGARLNDP    | 195                |           |             |
| Db | 121                   | PKELKGLETKLEKGISIRKKNELLFSEIEYMQKREITDLHNDNQYLRAKIAEHERA---    | 177                |           |             |
| Qy | 196                   | QOESSVTQGTTVYESGVSSHDSQHYNNRYIPVNLLPEPNOQFSGQDQPPQLQV          | 248                |           |             |
| Db | 178                   | OCOMNTMPGGSNVEVLPSPQEPS-----RNFTOVNALOPNHHYSRODOMALQV          | 226                |           |             |

```

RESULT 7
US-09-410-464-12
; Sequence 12, Application US/09410464
; Patent No. 6395892
; GENERAL INFORMATION:
; APPLICANT: Strauss et al.
; TITLE OF INVENTION: Floral homeotic
; TITLE OF INVENTION: poplar and other
; FILE REFERENCE: 53375
; CURRENT APPLICATION NUMBER: US/09/4
; CURRENT FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: 09/287,
; EARLIER FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Populus balsamifera subs
US-09-410-464-12

```

|    | Query Match                                                      | 60.9%            | Score 769.5;     | DB 4;     | Length 241; |
|----|------------------------------------------------------------------|------------------|------------------|-----------|-------------|
|    | Best Local Similarity                                            | 64.7%;           | Pred. No. 1e-69; |           |             |
|    | Matches 161;                                                     | Conservative 35; | Mismatches 44;   | Indels 9; | Gaps 3;     |
| QY | 1 MEEGSHDAESKKLGKGIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVAL         | 60               |                  |           |             |
| DQ | 1 MEYNESLESSPLRKLGRKGVEIKRIENTNRQVTFCRRSGLLKKAYELSVLCDAEVAL      | 60               |                  |           |             |
| QY | 61 VIFSTRGLYEYANNSVRGTIERYYKKACSDAVNPPSPYTEANTQQYQEASKLRQRIDIQ   | 120              |                  |           |             |
| DQ | 61 IVFSSRCRLRYEVSNDSVKSTIRERYKKASDSSNTGSSEANAQYOYOEAAKLRSOIGNLIQ | 120              |                  |           |             |

|    |     |                                                               |     |
|----|-----|---------------------------------------------------------------|-----|
| Qy | 121 | NSNRHIVGESLGSNPFKELNLEGRLEKGISRVRSKKNELLVAEIEYMQKREMELOQHNM   | 180 |
| Db | 121 | NSNRHMLGEALSSLVKELKSLEIRLEKGISRIRSKKNELLFAEIEYMQKREVDLHNNQ    | 180 |
| Qy | 181 | YLRAKTAEGARLNPDDQOESSVIOGTTVYVESGVSSHDSQHY-NNRYPVNLELPENQOFSG | 239 |
| Db | 181 | LLRAKTSENER--KQSMNLMPPGADFEI-----YQSQPYDSRNTSQVNGLQPAISHYSH   | 232 |
| Qy | 240 | QDQPPILQLV                                                    | 248 |
| Db | 233 | ODOMALOLV                                                     | 241 |

```

RESULT 8
US-08-460-512-5
; Sequence 5, Application US/08460512
; Patent No. 5744693
; GENERAL INFORMATION:
; APPLICANT: MEYEROWITZ, Elliot M.
; APPLICANT: YANOFKY, Martin F.
; APPLICANT: MA, Hong
; TITLE OF INVENTION: PLANTS HAVING ALTERED FLORAL DEVELOPMENT
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard F. Trecartin
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,512
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,278
; FILING DATE:
; APPLICATION NUMBER: US/07/956,694
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-57322/RFT
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 252 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-460-512-5

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|                       |        |                                                                               |          |            |     |        |      |
|-----------------------|--------|-------------------------------------------------------------------------------|----------|------------|-----|--------|------|
| Query Match           | 59.5%; | Score                                                                         | 752;     | DB         | 1;  | Length | 252; |
| Best Local Similarity | 63.2%; | Pred. No.                                                                     | 6.4e-68; |            |     |        |      |
| Matches               | 160;   | Conservative                                                                  | 33;      | Mismatches | 48; | Indels | 12;  |
| Gaps                  |        |                                                                               |          |            |     |        | 5;   |
| QY                    | 2      | EEGSSHDAESSKLGCKGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLGDAAEVALV                  | 61       |            |     |        |      |
|                       |        | :                                                                             |          |            |     |        |      |
| Db                    | 6      | ELGG--DSSPLRSGRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLGDAAEVALI                   | 62       |            |     |        |      |
|                       |        | :                                                                             |          |            |     |        |      |
| QY                    | 62     | IFSTRGRLYEYANNSVRGTIERYKKACSDAVNPSPVTANTQYQQEASKLRROIQTQN                     | 121      |            |     |        |      |
|                       |        | :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   : |          |            |     |        |      |
| Db                    | 63     | VFSRGRLYEYNSNVKGTIERYKKAISDNSNTGVSVAETNAQYQQEASAKLRQIOISIQN                   | 122      |            |     |        |      |
|                       |        | :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :     |          |            |     |        |      |
| QY                    | 122    | SNRHIVGSLGSLNFKEKLNLEGRLEKGISRVRSKKNELLVAETIYMQKREMLQHNMY                     | 181      |            |     |        |      |



Db 123 SNRLMGETIGSMSPKELNLEGRLETSITRIRSKKNELLFSEIDYMQKREVDLHNDNQI 182  
QY 182 LRAKIAEGARLNPDOQESSVIQTTVYESGV-SSHDQSOHY-NRNYIPVNLLEPNOQF-- 237  
Db 183 LRAKIAENERNNP---SISLMPGGSNYEQLMPPPTQSQPFDSRNYFQVAALQPNHHYS 239  
QY 238 --SQDQPPPLQLV 248  
Db 240 SAGRODQTALQLV 252

RESULT 9  
US-08-460-512-2  
; Sequence 2, Application US/08460512  
; Patent No. 5744693  
; GENERAL INFORMATION:  
; APPLICANT: MEYEROWITZ, Elliot M.  
; APPLICANT: YANOFKY, Martin F.  
; APPLICANT: MA, Hong  
; TITLE OF INVENTION: PLANTS HAVING ALTERED FLORAL DEVELOPMENT  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Richard F. Trecartin  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/460,512  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/293,278  
; FILING DATE:  
; APPLICATION NUMBER: US/07/956,694  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Trecartin, Richard F.  
; REGISTRATION NUMBER: 31,801  
; REFERENCE/DOCKET NUMBER: A-57322/RFT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 285 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-460-512-2

Query Match 59.5%; Score 752; DB 1; Length 285;  
Best Local Similarity 63.2%; Pred. No. 7.7e-68;  
Matches 160; Conservative 33; Mismatches 48; Indels 12; Gaps 5;

QY 2 EEEGSSHDAAESSKGLGRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVALY 61  
Db 39 ELGG---DSSPLRKSGRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVALI 95  
QY 62 IFSTRGRLEYANNVSGTIERKKACSDAVNPSPVTEANTQYQQEASKLRRQIRDION 121  
Db 96 VFSSRGRLEYNNVSGTIERKKAKSDNSNTGSAEINAQYQQEASAKLQQIISTON 155  
QY 122 SNRHIVGESLGNFKELNLEGRLEKISRVRSKKNELLVAEIEYMQKREMLQHNMY 181  
Db 156 SNRLMGETIGSMSPKELNLEGRLETSITRIRSKKNELLFSEIDYMQKREVDLHNDNQI 215

QY 182 LRAKIAEGARLNPDOQESSVIQTTVYESGV-SSHDQSOHY-NRNYIPVNLLEPNOQF-- 237  
Db 216 LRAKIAENERNNP---SISLMPGGSNYEQLMPPPTQSQPFDSRNYFQVAALQPNHHYS 272  
QY 238 --SQDQPPPLQLV 248  
Db 273 SAGRODQTALQLV 285

RESULT 10  
US-08-460-512-4  
; Sequence 4, Application US/08460512  
; Patent No. 5744693  
; GENERAL INFORMATION:  
; APPLICANT: MEYEROWITZ, Elliot M.  
; APPLICANT: YANOFKY, Martin F.  
; APPLICANT: MA, Hong  
; TITLE OF INVENTION: PLANTS HAVING ALTERED FLORAL DEVELOPMENT  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Richard F. Trecartin  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/460,512  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/293,278  
; FILING DATE:  
; APPLICATION NUMBER: US/07/956,694  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Trecartin, Richard F.  
; REGISTRATION NUMBER: 31,801  
; REFERENCE/DOCKET NUMBER: A-57322/RFT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 252 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-460-512-4

Query Match 59.5%; Score 751; DB 1; Length 252;  
Best Local Similarity 62.0%; Pred. No. 8.1e-68;  
Matches 158; Conservative 34; Mismatches 49; Indels 14; Gaps 5;

QY 1 MEEGSSHDAAESSKGLGRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVAL 60  
Db 5 MELGGES---SPQRKAGRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVAL 61  
QY 61 VIFSTRGRLEYANNVSGTIERKKACSDAVNPSPVTEANTQYQQEASKLRRQIRDIO 120  
Db 62 IVFSSRGRLEYNNVSGTIERKKAKSDNSNTGSAEINAQYQQEASAKLQQIISTIO 121  
QY 121 NSNRHIVGESLGNFKELNLEGRLEKISRVRSKKNELLVAEIEYMQKREMLQHNMM 180  
Db 122 NSNRQLMGETIGSMSPKELNLEGRLEDRSVNRIRSKKNELLFAEIDYMQKREVDLHNDNQ 181  
QY 181 YLRAKIAEGARLNPDOQESSVIQTTVYESGVSSHDQSOHY---NRNYIPVNLLEPNOQF 237

|                                                                              |     |                                                             |     |
|------------------------------------------------------------------------------|-----|-------------------------------------------------------------|-----|
| Db                                                                           | 182 | LLRAKIAENRRNPSM--SLMPGGSYEQ-IMPPQTQPQPFDSRNYFQVAALQPNHH     | 237 |
| Qy                                                                           | 238 | ----SGQDQPPLQLV                                             | 248 |
| Db                                                                           | 238 | YSSAGREDQTALQLV                                             | 252 |
| RESULT 11                                                                    |     |                                                             |     |
| US-09-410-464-16                                                             |     |                                                             |     |
| ; Sequence 16, Application US/09410464                                       |     |                                                             |     |
| ; Patent No. 6395892                                                         |     |                                                             |     |
| ; GENERAL INFORMATION:                                                       |     |                                                             |     |
| ; APPLICANT: Strauss et al.                                                  |     |                                                             |     |
| ; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in |     |                                                             |     |
| ; TITLE OF INVENTION: poplar and other plant species.                        |     |                                                             |     |
| ; FILE REFERENCE: 53375                                                      |     |                                                             |     |
| ; CURRENT APPLICATION NUMBER: US/09/410,464                                  |     |                                                             |     |
| ; CURRENT FILING DATE: 1999-10-01                                            |     |                                                             |     |
| ; EARLIER APPLICATION NUMBER: 09/287,700                                     |     |                                                             |     |
| ; EARLIER FILING DATE: 1999-04-06                                            |     |                                                             |     |
| ; EARLIER APPLICATION NUMBER: 60/080,851                                     |     |                                                             |     |
| ; EARLIER FILING DATE: 1998-04-06                                            |     |                                                             |     |
| ; NUMBER OF SEQ ID NOS: 24                                                   |     |                                                             |     |
| ; SOFTWARE: PatentIn Ver. 2.0                                                |     |                                                             |     |
| ; SEQ ID NO 16                                                               |     |                                                             |     |
| ; LENGTH: 238                                                                |     |                                                             |     |
| ; TYPE: PRT                                                                  |     |                                                             |     |
| ; ORGANISM: Populus balsamifera subsp. trichocarpa                           |     |                                                             |     |
| US-09-410-464-16                                                             |     |                                                             |     |
| Query Match 58.6%; Score 739.5; DB 4; Length 238;                            |     |                                                             |     |
| Best Local Similarity 65.5%; Pred. No. 1.1e-66;                              |     |                                                             |     |
| Matches 154; Conservative 34; Mismatches 36; Indels 11; Gaps 4;              |     |                                                             |     |
| Qy                                                                           | 11  | ESS--KKLGKGIETRIENTNRQVTFCRRNGLLKKAYELSVLCDAEVALVIFSTRGR    | 68  |
| Db                                                                           | 9   | ESSPLRLKRGCKVEIKRIENTNRQVTFCRRNGLLKKAYELSVLCDAEVALVIFSSRGR  | 68  |
| Qy                                                                           | 69  | LYEANNRSVRTIERYKKACSDAVNPSPVTEANTQYYQQEAASKLRQRIRDTONSNRHVG | 128 |
| Db                                                                           | 69  | LIEYSNNVKSTIERYKKACADSSNGSVSEANAQFYQQEAALKRSIGNLQNNSRNMLG   | 128 |
| Qy                                                                           | 129 | ESLGLNFKEKLNLGRLEKGISRVRSKKNELLVAEIYEMOKREMELOHNNMYLRAKIAE  | 188 |
| Db                                                                           | 129 | EELSALSVELKSLETKLEKGIRISKKNELLFAEIYEMOKREIDJHNNOQLLRAKIAE   | 188 |
| Qy                                                                           | 189 | GARLNPDQOESSVIQGTTVYESGVSSHDDQSQHY-NRNYIPVNLLPEPQQESGDQ     | 242 |
| Db                                                                           | 189 | NER---KRQHMLMPGGVNFET-----MQSQPFDSRNYSQVGNLPPANHPHEDQ       | 235 |
| RESULT 12                                                                    |     |                                                             |     |
| US-08-867-087B-13                                                            |     |                                                             |     |
| ; Sequence 13, Application US/08867087B                                      |     |                                                             |     |
| ; Patent No. 5990386                                                         |     |                                                             |     |
| ; GENERAL INFORMATION:                                                       |     |                                                             |     |
| ; APPLICANT: An, Gynheung                                                    |     |                                                             |     |
| ; TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT                   |     |                                                             |     |
| ; TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS                         |     |                                                             |     |
| ; NUMBER OF SEQUENCES: 70                                                    |     |                                                             |     |
| ; CORRESPONDENCE ADDRESS:                                                    |     |                                                             |     |
| ; ADDRESSEE: Kiarquist Sparkman Campbell Leigh &                             |     |                                                             |     |
| ; ADDRESSEE: Whinston, LLP                                                   |     |                                                             |     |
| ; STREET: One World Trade Center                                             |     |                                                             |     |
| ; STREET: 121 S.W. Salmon Street                                             |     |                                                             |     |
| ; STREET: Suite 1600                                                         |     |                                                             |     |
| ; CITY: Portland                                                             |     |                                                             |     |
| ; STATE: Oregon                                                              |     |                                                             |     |
| ; COUNTRY: United States of America                                          |     |                                                             |     |
| ; ZIP: 97204                                                                 |     |                                                             |     |
| ; COMPUTER READABLE FORM:                                                    |     |                                                             |     |
| ; MEDIUM TYPE: Disk, 3-1/2 inch                                              |     |                                                             |     |

```

; FILING DATE: June 2, 1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/323,449
; FILING DATE: October 14, 1994
; APPLICATION NUMBER: U.S. 08/485,981
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan E.
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 4630-47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
US-08-867-087B-11

```

|                       |        |                    |        |                |
|-----------------------|--------|--------------------|--------|----------------|
| Query Match           | 33.7%; | Score 426;         | DB 2;  | Length 241;    |
| Best Local Similarity | 40.4%; | Pred. No. 4.3e-35; |        |                |
| Matches               | 97;    | Conservative       | 49;    | Mismatches 64; |
|                       |        |                    | Indels | 30;            |
|                       |        |                    | Gaps   | 6;             |

|    |     |      |       |       |         |       |        |        |      |       |         |       |      |         |         |       |       |     |   |   |   |   |   |   |   |   |        |        |     |   |   |   |   |   |   |   |   |   |   |     |   |   |   |   |   |   |     |
|----|-----|------|-------|-------|---------|-------|--------|--------|------|-------|---------|-------|------|---------|---------|-------|-------|-----|---|---|---|---|---|---|---|---|--------|--------|-----|---|---|---|---|---|---|---|---|---|---|-----|---|---|---|---|---|---|-----|
| QY | 16  | LGRG | IEIK  | RIENT | NRQV    | TKRR  | NRGL   | LKAY   | ELSV | LCDA  | EVAL    | VIFST | RGR  | LYE-YAN | 74      |       |       |     |   |   |   |   |   |   |   |   |        |        |     |   |   |   |   |   |   |   |   |   |   |     |   |   |   |   |   |   |     |
| Db | 1   | MGRV | ELK   | RIEN  | KINR    | QVTF  | AKRR   | NRGL   | LKAY | ELSV  | LCDA    | EVALL | IFS  | RNGK    | LYECCSS | 60    |       |     |   |   |   |   |   |   |   |   |        |        |     |   |   |   |   |   |   |   |   |   |   |     |   |   |   |   |   |   |     |
| QY | 75  | NSVR | GTIER | YKK   | KACD    | AVNP  | PSVT-- | EANT   | OYYQ | QEASK | LRRQ    | IRDI  | QNSN | RHIV    | GESLG   | 132   |       |     |   |   |   |   |   |   |   |   |        |        |     |   |   |   |   |   |   |   |   |   |   |     |   |   |   |   |   |   |     |
| Db | 61  | SSML | KT    | LER   | YQK-CNY | GAPET | NIS    | TREALE | ISSQ | BYLKL | KARYEAL | QRSQ  | RNL  | GED     | LDLG    | 119   |       |     |   |   |   |   |   |   |   |   |        |        |     |   |   |   |   |   |   |   |   |   |   |     |   |   |   |   |   |   |     |
| QY | 133 | SLNF | ELKN  | LEGR  | LEK     | GIS   | RVR    | SKN    | ELL  | VAEI  | EVQ     | QKRE  | MELQ | HNN     | MYL     | RAKIA | EGARL | 192 |   |   |   |   |   |   |   |   |        |        |     |   |   |   |   |   |   |   |   |   |   |     |   |   |   |   |   |   |     |
| Db | 120 | PLNS | KE    | LES   | LER     | QD    | MSL    | KQIR   | STR  | Q     | MLD     | Q     | LT   | D       | LQ      | RKE   | HALNE | ANR | T | L | Q | R | M | E | G | S | Q      | L      | 179 |   |   |   |   |   |   |   |   |   |   |     |   |   |   |   |   |   |     |
| QY | 193 | NP   | Q     | Q     | E       | S     | S      | V      | I    | G     | T       | T     | V    | E       | S       | G     | V     | S   | S | H | D | S | Q | H | Y | N | R      | N----- | Y   | I | P | V | N | L | L | E | P | N | Q | O   | F | S | Q | D | Q | P | 243 |
| Db | 180 | NL   | Q     | W     | O       | O     | N      | A----- | Q    | D     | M       | G     | Y    | R       | O       | T     | T     | Q   | G | D | G | F | F | H | P | L | B----- | C      | E   | P | T | L | O | I | G | Y | N | D | P | 222 |   |   |   |   |   |   |     |

RESULT 14  
US-08-592-214A-8  
; Sequence 8, Application US/08592214A  
; Patent No. 5811536

```

; TELEFAX: (619) 535-8949
;
; INFORMATION FOR SEQ ID NO: 8:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 273 amino acids
;
; TYPE: amino acid
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
US-08-592-214A-8

```

Query Match 33.7%; Score 426; DB 2; Length 273;  
Best Local Similarity 38.0%; Pred. No. 5.3e-35;  
Matches 100; Conservative 48; Mismatches 81; Indels 34; Gaps 5;

[illegible]

```

RESULT 15
US-08-659-188-8
; Sequence 8, Application US/08659188
; Patent No. 6002069
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Seed Plants Exhibiting Induced
; TITLE OF INVENTION: Reproductive Development and
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESS: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,188
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1946
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-659-188-8

```

```
Query Match      33.7%; Score 426; DB 3; Length 273;
Best Local Similarity 38.0%; Pred. No. 5.3e-35;
Matches 100; Conservative 48; Mismatches 81; Indels 34; Gaps 5;

Qy 16 LGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGRLYEYANN 75
   :||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
Db 1  MGRGVQLKRIENKINRQVTFCKRRNGLLKKAEISVLCDAEVALVIFSPKGLYEYATD 60

Qy 76 SVRGTI----ERYKKACSDAVNPPSVTEANTQYQOEASKLRRQIRDIQNSNRHIVGESL 131
   | ||| | : : : | : | : | : | : | : | : | : | : | : | : |
Db 61 SRMDKILERYERYSAEKALISAESSEGN--WCHYEYRKLKAKIETIQCKHLMGEDL 117

Qy 132 GSLNPKELKNLEGRLEKIGSRVRSKKNELIVAEIYMQKREMEQLQHNMMYLRAKIAEGAR 191
   ||| ||| : || : : ||| : | : ||| : ||| : ||| : ||| : ||| :
Db 118 ESLNPKELQOLEQQDSSSLKHIRSRKSHLMAESISELQKKERSLOEENKALQKELAEK 177

Qy 192 -----LNPQQESSVIQGTIVYESGVSSHQDS---QHYNRYIPVNL----- 230
   : ||| : ||| : | : | : | : | : | : | : | : | : | : | :
Db 178 AVASRQQQQQQVQWQDQTHAQATSSSSSFMMRQDQQLPPPHNICFPPLTMGDRGEE 237

Qy 231 -----LEPNQQFSQDQPPQL 247
   : | || || | :
Db 238 LAAAAAQQQQLPGQAQPOLRI 260
```

Search completed: January 27, 2003, 12:46:49  
Job time : 14.5547 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2003, 12:42:53 ; Search time 14.5587 Seconds  
(without alignments)  
1637.600 Million cell updates/sec

Title: US-09-978-382A-4  
Perfect score: 1263  
Sequence: 1 MEEGSSHDAESSKLGK.....NLLEPNQFSGQDPPLQLV 248

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues 283224  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID     | Description        |
|------------|-------|-------------|--------|--------|--------------------|
| 1          | 1263  | 100.0       | 248    | A39534 | floral homeotic pr |
| 2          | 1050  | 83.1        | 246    | E39534 | floral homeotic pr |
| 3          | 1046  | 82.8        | 258    | G84858 | floral homeodomain |
| 4          | 806.5 | 63.9        | 248    | T03592 | floral homeotic pr |
| 5          | 798.5 | 63.2        | 248    | T07185 | floral homeotic pr |
| 6          | 794.5 | 62.9        | 242    | JQ2212 | pMADS3 protein - g |
| 7          | 793   | 62.8        | 247    | S60307 | fbp6 protein - gar |
| 8          | 781.5 | 61.9        | 239    | A44343 | promotes sex organ |
| 9          | 752   | 59.5        | 284    | T05033 | floral homeotic pr |
| 10         | 752   | 59.5        | 284    | A85214 | floral homeotic pr |
| 11         | 751   | 59.5        | 252    | A43484 | probable transcrip |
| 12         | 729.5 | 57.8        | 253    | S57586 | MADS-box regulator |
| 13         | 729   | 57.7        | 262    | T08039 | MADS-box protein - |
| 14         | 705   | 55.8        | 229    | T08040 | MADS-box protein - |
| 15         | 698.5 | 55.3        | 236    | S59480 | MADS-box protein 3 |
| 16         | 695.5 | 55.1        | 254    | T10185 | MADS-box protein C |
| 17         | 678   | 53.7        | 230    | T04000 | MADS-box protein A |
| 18         | 670   | 53.0        | 222    | T01700 | hypothetical prote |
| 19         | 646.5 | 51.2        | 222    | S51934 | MADS-box protein d |
| 20         | 641   | 50.8        | 286    | JQ2289 | floral homeotic pr |
| 21         | 627.5 | 49.7        | 265    | T02261 | MADS box protein - |
| 22         | 582.5 | 46.1        | 258    | PQ0770 | floral homeotic pr |
| 23         | 474   | 37.5        | 261    | S51935 | probable MADS-box  |
| 24         | 467   | 37.0        | 261    | T09603 | MADS-box protein 3 |
| 25         | 461.5 | 36.5        | 242    | T09571 | MADS box protein M |
| 26         | 460   | 36.4        | 242    | T10486 | MADS box protein - |
| 27         | 450.5 | 35.7        | 250    | T04167 | MADS box protein - |
| 28         | 447.5 | 35.4        | 255    | T03398 | MADS box protein - |
| 29         | 441   | 34.9        | 255    | T03408 | MADS box protein - |

ALIGNMENTS

RESULT 1

A39534  
floral homeotic protein AGL1 [similarity] - Arabidopsis thaliana  
N:Alternate names: agamous-like 1 AGL1; Shatterproof 1 SHP1; T20N10.130  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 09-Jun-2000  
C:Accession: A39534; T49161  
R:Ma, H.; Yanofsky, M.F.; Meyerowitz, E.M.  
Genes Dev. 5, 484-495, 1991  
A:Title: AGL1-AGL6, an Arabidopsis gene family with similarity to floral homeotic and  
A:Reference number: A39534; MUID:91160981; PMID:1672119  
A:Accession: A39534  
A:Molecule type: DNA  
A:Residues: 1-248 <MAA>  
A:Cross-references: GB:M55550; NID:g166587; PIDN:AAA32730.1; PID:g166588  
R:D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Rudd, S.  
submitted to the Protein Sequence Database, April 2000  
A:Reference number: 225017  
A:Accession: T49161  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-248 <DAN>  
A:Cross-references: EMBL:AL353032; GSPDB:GN00061; ATSP:T20N10.130  
A:Experimental source: cultivar Columbia; BAC clone T20N10  
C:Genetics:  
A:Gene: ATSP:T20N10.130  
A:Map position: 3  
A:Introns: 76/2; 103/3; 124/2; 157/3; 171/3; 185/3  
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain ho  
C:Keywords: DNA binding; nucleus; transcription regulation  
F:17-72/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 100.0%; Score 1263; DB 2; Length 248;  
Best Local Similarity 100.0%; Pred. No. 3.4e-81;  
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEEGSSHDAESSKLGKLGKLEIKRIENTTNRQVTFCKRRNGLLKRAYELSVLCDAEVAL 60  
Db 1 MEEGSSHDAESSKLGKLGKLEIKRIENTTNRQVTFCKRRNGLLKRAYELSVLCDAEVAL 60  
QY 61 VIFSTRGRLYEYANNSVGRGTIERYKKACSDAVNPPSPVTEANTQYYQOEASKLRQIRDIQ 120  
Db 61 VIFSTRGRLYEYANNSVGRGTIERYKKACSDAVNPPSPVTEANTQYYQOEASKLRQIRDIQ 120  
QY 121 NSNRHIVGESLGSNFKELKNLEGRLEKIGISRVRSKKNELVAEIEYMQKREMELOHNMM 180  
Db 121 NSNRHIVGESLGSNFKELKNLEGRLEKIGISRVRSKKNELVAEIEYMQKREMELOHNMM 180  
QY 181 YLRAKTAEGARLNPDQOESSVIOGTTVYESGVSSHDSQSHYNNRNYIPVNNLLEPNQOFSGQ 240  
Db 181 YLRAKTAEGARLNPDQOESSVIOGTTVYESGVSSHDSQSHYNNRNYIPVNNLLEPNQOFSGQ 240

QY 241 DOPPLQLV 248  
|||||

Db 241 DOPPLQLV 248

## RESULT 2

E39534

floral homeotic protein AGL5 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 24-Sep-1999

C:Accession: E39534

R:Ma, H.; Yanofsky, M.F.; Meyerowitz, E.M.

Genes Dev. 5, 484-495, 1991

A:Title: AGL1-AGL6, an Arabidopsis gene family with similarity to floral homeotic and tr

A:Reference number: A39534; MUID:91160981; PMID:1672119

A:Accession: E39534

A:Molecule type: DNA

A:Residues: 1-246 &lt;MAA&gt;

A:Cross-references: GB:M55553; NID:g166595; PIDN:AAA32735.1; PID:g166596

C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol

C:Keywords: DNA binding; nucleus; transcription regulation

F:17-72/Domain: serum response factor DNA-binding domain homology &lt;SRF&gt;

Query Match 83.1%; Score 1050; DB 2; Length 246;

Best Local Similarity 85.5%; Pred. No. 2.5e-66;

Matches 212; Conservative 12; Mismatches 22; Indels 2; Gaps 1;

QY 1 MEEGSSHDAESSKKLGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVAL 60

||| | : |||||

Db 1 MEGGASNEVAESSKKIGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVAL 60

QY 61 VIFSTRGRLYEYANNSVRGTIERYKKACSDAVNPSPVTEANTQYYQOEASKLRQIRDIQ 120

|||||

Db 61 VIFSTRGRLYEYANNSVRGTIERYKKACSDAVNPSPVTEANTQYYQOEASKLRQIRDIQ 120

QY 121 NSNRHIVGESLGNFKELKNLEGRLEKIGISRVRSKKNELVAEIEYMQKREMELOHNNM 180

| | | | : |||||

Db 121 NUNRHILGESLGNFKELKNLEGRLEKIGISRVRSKKNELVAEIEYMQKREMELOHNNM 180

QY 181 YLRKIAEGARLNPDOQESSVIQGTIVYESGVSSHQSOHYNNRNIIPVNLLEPNQOFSQ 240

|||||

Db 181 YLRKITE--RTGLQQOESSVIHQGTIVYESGVSSHQSOHYNNRNIIPVNLLEPNQOFSQ 238

QY 241 DOPPLQLV 248

|||||

Db 239 DOPPLQLV 246

## RESULT 3

G84858

floral homeodomain transcription factor (AGL5) [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 16-Feb-2001

C:Accession: G84858

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: G84858

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-258 &lt;STO&gt;

A:Cross-references: GB:AE002093; NID:g4512687; PIDN:AAD21741.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g42830

A:Map position: 2

C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol

Query Match

Best Local Similarity 82.8%; Score 1046; DB 2; Length 258;

Matches 211; Conservative 12; Mismatches 22; Indels 2; Gaps 1;









```

Db      1 MGRGKIEIKRIENTNTRQVTFCKRRNGLLKKAYELSVLCDAEVALIVFSSRGLIYEYSNN 60

Qy     76 SVRGTIERYKKACSDAVNPSPVTETANTQYQQEQEASKLRQRIRDIONSN---RHIVGESL 131
       : : ||||| : | | | | | : | | : | | | | : | | | | | | | | | | | | | | | |
Db     61 SIKTTIERYKKACSDSSATTSSTVELNTQYQQESAKLRQOIQMLQNSNLVRHLMGDSL 120

Qy    132 GSLNFKEKLNLEGRLEKGISRVRSKKNELLVAETIEMQKREMLEQHNNMYLRAKIAEGAR 191
       : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    121 SALTVKELQOLENRLERGITIRSKHEMLAEITYLOKREILEENVCIRT KIAEVER 180

Qy    192 LNPDOQESSVIQGTTYVESGVSSHDSQSHYRNYPVNLP- --NQQFSQGDPPLQL 247
       : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db    181 V----QQANWVGQEL-----NAIQALANSRNFFSPNMEPAGVPVSYSHQDKMHL 228


RESULT 15
MADS-box protein 3 - rice
C:Species: Oryza sativa (rice)
C>Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 28-May-1999
C:Accession: S59480
R;Kang, H.G.; Noh, Y.S.; Chung, Y.Y.; Costa, M.A.; An, K.; An, G.
Plant Mol. Biol. 29, 1-10, 1995
A>Title: Phenotypic alterations of petal and sepal by ectopic expression of a rice MAD5
A:Reference number: S59480; MUID:96017609; PMID:7579155
A:Accession: S59480
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-236 <KAN>
A:Cross-references: GB:L37528; NID:g886404; PIDN:AAA99964.1; PID:g886405
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homology
F;2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match          55.3%; Score 698.5; DB 2; Length 236;
Best Local Similarity 59.7%; Pred. No. 8.2e-42;
Matches 141; Conservative 47; Mismatches 37; Indels 11; Gaps 5;

Qy    16 LRGKIEIKRIENTNTRQVTFCKRRNGLLKKAYELSVLCDAEVALIVFSTRGLIYEYANN 75
       : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     1 MGRGKIEIKRIENTNTRQVTFCKRRNGLLKKAYELSVLCDAEVALIVFSSRGLIYEYANN 60

Qy    76 SVRGTIERYKKACSDAVNPSPVTETANTQYQQEQEASKLRQRIRDIONSN-RHIVGESLSL 134
       : | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     61 SVKSIVERYKKANSDTSNCGTVAEVNAHQYQQESSKLKROQISSLQANASRTIVGDSINTM 120

Qy   135 NFKEKLNLEGRLEKGISRVRSKKNELLVAETIEMQKREMLEQHNNMYLRAKIAEGARLNP 194
       : : | | : | | | | | : | | | | | | | | | | | | | | | | | | | | | |
Db   121 SLRDLKQOVNRLKGIARKNKNELLYAEVEYMQRVEYLQNNDNMYLRSKVVENER--- 177

Qy   195 DQQESSVI--QGTTYVESGVSSHDSQSHYRNYPVNLPNQOFSGDQP-PQLQL 247
       | | : : : | : | : : : | : : : : | : : : : | : : : : | : : : : |
Db   178 GQQLPMMGAASTSEYDHMVN----NPYDSRNFLQVNIIMQOPQHYAHQLQPTTLQL 229


Search completed: January 27, 2003, 12:46:15
Job time : 14.5587 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 27., 2003, 12:39:28 ; Search time 31.6275 seconds  
(without alignments)  
1044.854 Million cell updates/sec

Title: US-09-978-382A-4  
Perfect score: 1263  
Sequence: 1 MEEGSSHDAESSKILGRK.....NLLEPNQFSGDQPPPLQLV 248

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues  
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_101002:\*

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2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*  
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*  
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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID          | Description        |
|------------|-------|-------------|--------|-------------|--------------------|
| 1          | 1263  | 100.0       | 248    | 20 AAW80999 | Arabidopsis AGL1 p |
| 2          | 1263  | 100.0       | 248    | 21 AAG09411 | Arabidopsis thalia |
| 3          | 1050  | 83.1        | 246    | 20 AAW81000 | Arabidopsis AGL5 p |
| 4          | 1046  | 82.8        | 258    | 21 AAG32583 | Arabidopsis thalia |
| 5          | 830.5 | 65.8        | 251    | 17 AAR99633 | Eucalyptus AGE-1 p |
| 6          | 769.5 | 60.9        | 241    | 21 AAY58656 | Poplar PTAG-1 flor |
| 7          | 769.5 | 60.9        | 241    | 22 AAB68437 | Amino acid sequenc |
| 8          | 769.5 | 60.9        | 241    | 23 ABG30867 | Poplar floral home |
| 9          | 752   | 59.5        | 300    | 21 AAG52721 | Arabidopsis thalia |
| 10         | 739.5 | 58.6        | 238    | 21 AAY58657 | Poplar PTAG-2 flor |

|    |       |      |     |             |                    |
|----|-------|------|-----|-------------|--------------------|
| 11 | 739.5 | 58.6 | 238 | 22 AAB68438 | Amino acid sequenc |
| 12 | 739.5 | 58.6 | 238 | 23 ABG30868 | Poplar floral home |
| 13 | 722   | 57.2 | 221 | 21 AAY44804 | Petunia hybrida ne |
| 14 | 722   | 57.2 | 221 | 21 AAY58648 | Petunia nectary-sp |
| 15 | 712.5 | 56.4 | 264 | 23 ABG60988 | Novel floral meris |
| 16 | 695.5 | 55.1 | 257 | 21 AAG33135 | Zea mays protein f |
| 17 | 695.5 | 55.1 | 260 | 21 AAG33134 | Zea mays protein f |
| 18 | 695.5 | 55.1 | 283 | 21 AAG33133 | Zea mays protein f |
| 19 | 689.5 | 54.6 | 268 | 23 ABG60931 | Novel floral meris |
| 20 | 680   | 53.8 | 277 | 21 AAG16689 | Arabidopsis thalia |
| 21 | 680   | 53.8 | 277 | 21 AAG40212 | Arabidopsis thalia |
| 22 | 679.5 | 53.8 | 185 | 21 AAB32638 | Eucalyptus grandis |
| 23 | 678   | 53.7 | 230 | 21 AAG16690 | Arabidopsis thalia |
| 24 | 678   | 53.7 | 230 | 21 AAG40213 | Arabidopsis thalia |
| 25 | 663.5 | 52.5 | 229 | 17 AAR99637 | Eucalyptus AGE-2 p |
| 26 | 651.5 | 51.6 | 222 | 21 AAB26795 | Plant reproductive |
| 27 | 628   | 49.7 | 133 | 21 AAG07156 | Arabidopsis thalia |
| 28 | 626.5 | 49.6 | 268 | 21 AAG43856 | Zea mays protein f |
| 29 | 555   | 43.9 | 161 | 21 AAB33229 | Eucalyptus grandis |
| 30 | 503   | 39.8 | 142 | 21 AAG12611 | Zea mays protein f |
| 31 | 503   | 39.8 | 155 | 21 AAG12609 | Zea mays protein f |
| 32 | 486   | 38.5 | 122 | 21 AAG37576 | Arabidopsis thalia |
| 33 | 473.5 | 37.5 | 260 | 23 ABG60946 | Novel floral meris |
| 34 | 467   | 37.0 | 261 | 19 AAW48623 | Pinus radiata cone |
| 35 | 461.5 | 36.5 | 242 | 19 AAW48622 | Pinus radiata cone |
| 36 | 458   | 36.3 | 205 | 23 ABG60922 | Novel floral meris |
| 37 | 453   | 35.9 | 260 | 21 AAG17603 | Arabidopsis thalia |
| 38 | 452.5 | 35.8 | 181 | 21 AAB33310 | Pinus radiata tran |
| 39 | 451.5 | 35.7 | 260 | 21 AAG40277 | Arabidopsis thalia |
| 40 | 450.5 | 35.7 | 250 | 21 AAO17679 | Plant flowering ti |
| 41 | 447   | 35.4 | 269 | 21 AAY84911 | Amino acid sequenc |
| 42 | 445   | 35.2 | 281 | 21 AAG29741 | Arabidopsis thalia |
| 43 | 442   | 35.0 | 250 | 21 AAG17604 | Arabidopsis thalia |
| 44 | 440.5 | 34.9 | 251 | 21 AAG40278 | Arabidopsis thalia |
| 45 | 431   | 34.1 | 241 | 17 AAR96962 | NLMADS3 protein.   |

ALIGNMENTS

RESULT 1

|          |                                                                                                                                      |
|----------|--------------------------------------------------------------------------------------------------------------------------------------|
| AAW80999 |                                                                                                                                      |
| ID       | AAW80999 standard; Protein; 248 AA.                                                                                                  |
| XX       |                                                                                                                                      |
| AC       | AAW80999;                                                                                                                            |
| XX       |                                                                                                                                      |
| DT       | 10-MAY-1999 (first entry)                                                                                                            |
| XX       |                                                                                                                                      |
| DE       | Arabidopsis AGL1 polypeptide.                                                                                                        |
| XX       |                                                                                                                                      |
| KW       | AGL1-like gene; agamous-like 1 gene; seed dispersal; dehiscence;                                                                     |
| KW       | transgenic plant.                                                                                                                    |
| XX       |                                                                                                                                      |
| OS       | Arabidopsis thaliana.                                                                                                                |
| XX       |                                                                                                                                      |
| PN       | WO900502-A1.                                                                                                                         |
| XX       |                                                                                                                                      |
| PD       | 07-JAN-1999.                                                                                                                         |
| XX       |                                                                                                                                      |
| PF       |                                                                                                                                      |
| XX       | 25-JUN-1998; 98WO-US13208.                                                                                                           |
| XX       |                                                                                                                                      |
| PR       | 28-APR-1998; 98US-0067800.                                                                                                           |
| PR       | 27-JUN-1997; 97US-0051030.                                                                                                           |
| XX       |                                                                                                                                      |
| PA       | (REGC ) UNIV CALIFORNIA.                                                                                                             |
| XX       |                                                                                                                                      |
| PI       | Ferrandiz C, Yanofsky MF;                                                                                                            |
| XX       |                                                                                                                                      |
| DR       | WPI; 1999-095747/08.                                                                                                                 |
| DR       | N-PSDB; AAV99857, AAV99859.                                                                                                          |
| XX       |                                                                                                                                      |
| PT       | Use of agamous-like nucleic acids - useful for the production of transgenic seed plants in which dehiscence is modified resulting in |



PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.

PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159638.  
PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160768.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

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Best Local Similarity 100.0%; Pred. No. 5.6e-116;  
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEEGSSHDAESSKLGKRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVAL 60  
Db 1 MEEGSSHDAESSKLGKRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVAL 60  
QY 61 VIFSTRGRLYEYANNSVRGTIERYKKACSDAVNPPSVTEANTQYYQOEASKLRRIQ 120  
Db 61 VIFSTRGRLYEYANNSVRGTIERYKKACSDAVNPPSVTEANTQYYQOEASKLRRIQ 120  
QY 121 NSNRHIVGESLGNFKELKNLEGRLEKGISRVRSKKNELLVAEIEYMQKREMELOHNNM 180  
Db 121 NSNRHIVGESLGNFKELKNLEGRLEKGISRVRSKKNELLVAEIEYMQKREMELOHNNM 180  
QY 181 YLRAKIAEGARLNPDQESSVIOGTTVYESGVSSHDSQSHYNNRNYIPVNLLPNOQFSGQ 240  
Db 181 YLRAKIAEGARLNPDQESSVIOGTTVYESGVSSHDSQSHYNNRNYIPVNLLPNOQFSGQ 240  
QY 241 DQPPLQLV 248  
Db 241 DQPPLQLV 248

RESULT 3  
AAW81000  
ID AAW81000 standard; Protein; 246 AA.  
XX  
AC AAW81000;  
XX  
DT 10-MAY-1999 (first entry)  
XX  
DE Arabidopsis AGL5 polypeptide.  
XX  
KW AGL5-like gene; agamous-like 5 gene; seed dispersal; dehiscence;  
KW transgenic plant.  
OS Arabidopsis thaliana.  
XX  
PN WO9900502-A1.  
XX

PD 07-JAN-1999.  
XX 25-JUN-1998; 98WO-US13208.  
XX 28-APR-1998; 98US-0067800.  
PR 27-JUN-1997; 97US-0051030.  
XX (REGC ) UNIV CALIFORNIA.  
PA  
XX Ferrandiz C, Yanofsky MF;  
XX WPI; 1999-095747/08.  
DR N-PSDB; AAV99858, AAV99860.  
XX  
XX Use of agamous-like nucleic acids - useful for the production of  
PT transgenic seed plants in which dehiscence is modified resulting in  
PT delayed seed dispersal  
XX  
PS Disclosure; Page 91-92; 126pp; English.  
XX  
CC This is the deduced amino acid sequence of an Arabidopsis  
CC agamous-like 5 (AGL5) polypeptide that is involved in the  
CC regulation of dehiscence. A cDNA clone encoding AGL5 is provided  
CC in AAV99860, and a genomic clone in AAV99858. The invention provides a  
CC transgenic seed plant, such as an agl1 and agl5 double mutant, that  
CC is characterised by delayed seed dispersal due to suppression of  
CC AGL1 (see AAW80999) and AGL5 expression. The invention also provides  
CC a gene, that confer selective expression upon an operatively linked  
CC nucleic acid molecule in the valve margin or dehiscence zone of a  
CC Brassicaceae, such as rapeseed, and members of the Fabaceae, such  
CC as soybean, pea, lentil and bean. A plant expression vector  
CC comprising a dehiscence zone-selective regulatory element, and a  
CC kit for producing the transgenic seed plants are also provided.  
XX  
SQ Sequence 246 AA;  
  
Query Match 83.1%; Score 1050; DB 20; Length 246;  
Best Local Similarity 85.5%; Pred. No. 5.2e-95;  
Matches 212; Conservative 12; Mismatches 22; Indels 2; Gaps 1;  
  
QY 1 MEEGSSHDAESSKLGKRGKIEIKRIENTNRQVTFCKRRNGLLKAYELSVLCDAEVAL 60  
Db 1 MEGGASNEVAESSKKGKIEIKRIENTNRQVTFCKRRNGLLKAYELSVLCDAEVAL 60  
  
QY 61 VIFSTRGRLYEYANNVSRGTERYKKACSDAVNPPTSVEANTQYQOEASKLRQIRDIQ 120  
Db 61 VIFSTRGRLYEYANNVSRGTERYKKACSDAVNPPTITEANTQYQOEASKLRQIRDIQ 120  
  
QY 121 NSNRHIVGESLGNPKELKNLEKIGISRVRSKKNELLVAEIYMQKREMELOHNMM 180  
Db 121 NLNRHILGESLGNPKELKNLESRLKIGISRVRSKKHMLVAEIEYMQKREIELQNDNM 180  
  
QY 181 YLRAKTAEAGRLNPQQESSVIGQTTVYESGVSHDQSQHYNRNYPVNLLEPNQOQFSGQ 240  
Db 181 YLRSKITE--RTGLQQOQESSVHQGTIVYESGVTSHQSGQYNNRYIAVNLLEPNQNSSNQ 238  
  
QY 241 DQPPLQLV 248  
Db 239 DQPPLQLV 246  
  
RESULT 4  
AAG32583  
ID AAG32583 standard; Protein; 258 AA.  
XX  
AC AAG32583;  
XX  
DT 17-OCT-2000 (first entry)  
XX Arabidopsis thaliana protein fragment SEQ ID NO: 39337.  
DE  
XX

KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
XX termination sequence.  
OS Arabidopsis thaliana.  
XX  
XX EPI033405-A2.  
PN  
XX 06-SEP-2000.  
PD  
XX  
PF 25-FEB-2000; 2000EP-0301439.  
XX  
PR 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 23-APR-1999; 99US-0130891.  
PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 06-MAY-1999; 99US-0132487.  
PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
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PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.



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| PR                                                             | 21-JUL-1999; | 99US-0144814.                                                   |
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| PR                                                             | 20-AUG-1999; | 99US-0149723.                                                   |
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| PR                                                             | 23-AUG-1999; | 99US-0149930.                                                   |
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| PR                                                             | 04-OCT-1999; | 99US-0157117.                                                   |
| PR                                                             | 05-OCT-1999; | 99US-0157753.                                                   |
| PR                                                             | 06-OCT-1999; | 99US-0157865.                                                   |
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| PR                                                             | 14-OCT-1999; | 99US-0159329.                                                   |
| PR                                                             | 14-OCT-1999; | 99US-0159330.                                                   |
| PR                                                             | 14-OCT-1999; | 99US-0159331.                                                   |
| PR                                                             | 14-OCT-1999; | 99US-0159637.                                                   |
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| PR                                                             | 28-OCT-1999; | 99US-0161920.                                                   |
| PR                                                             | 28-OCT-1999; | 99US-0161992.                                                   |
| PR                                                             | 28-OCT-1999; | 99US-0161993.                                                   |
| PR                                                             | 29-OCT-1999; | 99US-0162142.                                                   |
| Query Match 82.8%; Score 1046; DB 21; Length 258;              |              |                                                                 |
| Best Local Similarity 85.4%; Pred. No. 1.4e-94;                |              |                                                                 |
| Matches 211; Conservative 12; Mismatches 22; Indels 2; Gaps 1; |              |                                                                 |
| QY                                                             | 1            | MEEGSSHDAESSKKLGRGKIEIKRIENTTNRQVTFCKRRNGLLKAYELSVLCDAEVAL 60   |
| Db                                                             | 1            | MEGGASNEVAESSKKIGRGKIEIKRIENTTNRQVTFCKRRNGLLKAYELSVLCDAEVAL 60  |
| QY                                                             | 61           | VIFSTRGRLYEYANNVSRGTIERYKKACSDAVNPPSVTEANTQYQOEASKLRRIQ 120     |
| Db                                                             | 61           | VIFSTRGRLYEYANNVSRGTIERYKKACSDAVNPPPTITEANTQYQOEASKLRRIQ 120    |
| QY                                                             | 121          | NSNRHIVGESLGNFKELKNLEGRLEKGISRVRSKKNELLVAEIEYMQREMELOHNNM 180   |
| Db                                                             | 121          | NLNRHILGESLGNFKELKNLESRLKGISRVRSKKHEMLVAEIEYMQREIEQNDNM 180     |
| QY                                                             | 181          | YLRAKIAEGARLNPDQOESSVIOGTTVYESGVSHDQSOHYNRNYPVNLLEPNQOFSQ 240   |
| Db                                                             | 181          | YLRSKITE--RTGLQQOESSVIHQGTVYESGVTSHQSGQYNNRYIAVNLLLEPNQSSNQ 238 |
| QY                                                             | 241          | DQPPLQL 247                                                     |
| Db                                                             | 239          | DQPPLQL 245                                                     |
| RESULT 5                                                       |              |                                                                 |

AAR99633  
ID AAR99633 standard; Protein; 251 AA.  
XX AC AAR99633;  
XX DT 01-OCT-1996 (first entry)  
XX DE Eucalyptus AGE-1 protein.  
XX KW Eucalyptus; reproductive gene; AGE1; Arabidopsis; agamous gene;  
KW Antirrhinum; plena gene; sterility; fertility; forest tree;  
KW transgenic plant; flower development; antisense; ribozyme.  
XX OS Eucalyptus globulus.  
XX FH Key Location/Qualifiers  
FT Region 18..73  
FT /label= MADS\_box  
XX AU9539013-A.  
XX PD 30-MAY-1996.  
XX PF 22-NOV-1995; 95AU-0039013.  
XX PR 22-NOV-1994; 94AU-0009589.  
XX PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
XX PI Dennis ES, Harcourt RL, Kyozyuka J, Llewellyn D;  
PI Peacock WJ, Southerton S;  
XX DR WPI; 1996-278411/29.  
DR N-PSDB; AAT34428.  
XX Eucalyptus reproductive genes - useful for prodn. of sterile  
PT Eucalyptus trees useful for establishing wood lot plantations or in  
PT re-forestation projects  
XX PS Disclosure; Page 29-30; 60pp; English.  
XX AGE-1 protein (AAR99633) is the product of a cDNA clone, AGE1  
CC (AAT34428), isolated from Eucalyptus globulus cDNA on the basis of  
CC its homology to the Arabidopsis agamous (AG) and Antirrhinum plena  
CC (PLE) flower development genes. AGE-1 shows 68% homology to AG and  
CC 75% homology to PLE protein. AGE1 is very highly expressed in  
CC mature flower buds. A related protein, AGE-2 (AAR99637), was also  
CC identified. Antisense or ribozyme constructs of AGE, or of FLE2 and  
CC SOE genes (see also AAT34426 and AAT34429-31), can be used to produce  
CC sterile transgenic Eucalyptus trees by minimising inflorescence.  
XX Sequence 251 AA:  
SQ  
Query Match 65.8%; Score 830.5; DB 17; Length 251;  
Best Local Similarity 67.8%; Pred. No. 2.2e-73;  
Matches 173; Conservative 30; Mismatches 41; Indels 11; Gaps 4;  
QY 1 MEEGSSHDAESSKKL-GRGKIEIKRIENTNTRQVTFCKRRNGLLKAYELSVLCDAEVA 59  
DB 1 MEPPSEASEASQKRIGGRGKIEIKRIENTNTRQVTFCKRRNGLLKAYELSVLCDAEVA 60  
QY 60 LVIFSTRGRLEYANNVSRGTERYKKACSDAVNPPSVTEANTQYVQOEASKLRQIRDI 119  
DB 61 LVIFSSRGRLEYANNVSRGTERYKKASDSSHPOSVSEVNTQFYQOEASKLRQIREI 120  
QY 120 QNSNRHIVGESLGSNFKELNLEGRLEKGISRVRSKKNELLVAETIYMQKREMELOHNN 179  
DB 121 QVSNRHLIGEGISDLSPKDLKNLESLEKISRVRSKKNEMLFAETIYMQKREIELQND 180  
QY 180 MYLRAKTAEGARLNPDQOESS-----VIQGTTVYESGVSSHDQSQHYNNRNPVNLLEPN 234  
DB 181 MYLRAKTAENERAQOQQOQSGSDHFFNNMPPGSSSVYEALPS----QPAYDRNPLQVNVLEPN 236

QY 235 -QQFSGQDQPPLQLV 248  
DB 237 HQSYSRSDHTALQLV 251  
RESULT 6  
AAY58656  
ID AAY58656 standard; Protein; 241 AA.  
XX AC AAY58656;  
XX DT 11-APR-2000 (first entry)  
XX DE Poplar PTAG-1 floral homeotic gene-encoded protein.  
XX KW Poplar; PTAG-1; floral homeotic gene; transgenic plant; sterility;  
KW fertility.  
XX OS Populus balsamifera subsp. trichocarpa.  
XX FH Key Location/Qualifiers  
FT Domain 17..33  
FT /note= "MADS domain"  
FT Domain 106..172  
FT /note= "K domain"  
XX CA2227940-A1.  
XX PD 06-OCT-1999.  
XX PF 07-APR-1998; 98CA-2227940.  
XX PR 06-APR-1998; 98US-0080851.  
XX PA (UYOR-) UNIV OREGON HEALTH SCI.  
XX Rottmann WH, Brunner AM, Sheppard LA, Strauss SH;  
XX WPI; 2000-106662/10.  
DR N-PSDB; AAZ57946, AAZ57947.  
XX Nucleic acid from Populus trichocarpa genes, useful for producing  
PT transgenic plants, particularly trees, with modified fertility  
PT characteristics such as sterility -  
XX Claim 31; Page 67-68; 92pp; English.  
XX The present sequence is that of the novel PTAG-1 protein of poplar  
CC (Populus balsamifera subsp. trichocarpa), as deduced from newly  
CC isolated gene and cDNA sequences (see AAZ57946-47). PTAG-1 is 1  
CC of 4 novel floral homeotic genes identified in this poplar species.  
CC It is a homologue of AGAMOUS and is expressed in floral tissues.  
CC PTAG-1 contains a MADS domain and a K-domain. The invention  
CC provides nucleic acid sequences of the 4 novel Populus genes, the  
CC corresponding cDNA sequences (see AAZ47942-49) and deduced amino acid  
CC sequences (see AAY58454-57). It also provides methods of using the  
CC gene and cDNA sequences to produce genetically engineered Populus  
CC and other trees having modified fertility characteristics, including  
CC sterility. Genetic constructs useful in producing genetically  
CC engineered Populus and other trees include antisense versions of  
CC PTAG-1, dominant negative mutants, and constructs useful for sense  
CC suppression. Sterile trees allow increased wood yield and a  
CC reduction in the production of allergens such as pollen.  
XX Sequence 241 AA:  
SQ  
Query Match 60.9%; Score 769.5; DB 21; Length 241;  
Best Local Similarity 64.7%; Pred. No. 2.2e-67;  
Matches 161; Conservative 35; Mismatches 44; Indels 9; Gaps 3;  
QY 1 MEEGSSHDAESSKKLGRGKIEIKRIENTNTRQVTFCKRRNGLLKAYELSVLCDAEVAL 60  
DB 1 MEYQNESLESSPLRLGRGKVEIKRIENTNTRQVTFCKRRSGLLKAYELSVLCDAEVAL 60



XX Disclosure; Column 67-70; 46pp; English.

PS The invention relates to an isolated nucleic acid molecule especially a

XX protein transduction domain (PTD) promoter: (i) that hybridises under

CC wash conditions of 0.2 x SSC (saline sodium citrate), 0.1 %SDS (sodium

CC dodecyl sulphate) at 65 plusOC to nucleotides or (ii) comprising 35

CC consecutive nucleotides of the PTD gene. PTD is a floral homeotic

CC gene and is the homologue of DEFICIENS. Also includes are a recombinant

CC nucleic acid comprising the PTD promoter, a cell transformed with

CC the recombinant nucleic acid and a transgenic plant comprising the

CC expression of genes such as cytotoxins, that are employed in genetic

CC ablation strategies to produce trees having modified fertility

CC characteristics, including sterility. Genetic constructs comprising

CC antisense versions or dominant negative mutants of PTD are useful in

CC producing genetically engineered Poplars and other trees, and for sense

CC suppression. Also disclosed are 3 other homeotic genes PTLF, PTAG-1

CC and PTAG-2 (none are defined). The present sequence is the PTAG-1

CC protein.

XX Sequence 241 AA;

SQ Query Match 60.9%; Score 769.5; DB 23; Length 241;

Best Local Similarity 64.7%; Pred. No. 2.2e-67;

Matches 161; Conservative 35; Mismatches 44; Indels 9; Gaps 3;

Qy 1 MEEGSSHDAESSKLGKRGKIEIKRIENTNRQVTFCKRRNGLLKKAYELSVLCDAEVAL 60

Db 1 MEYQNESLESSPLRLGKRGKVEIKRIENTNRQVTFCKRRSGLLKKAYELSVLCDAEVAL 60

Qy 61 VIFSTRGLYAYANNSVRGTYERYKKACSDAVNPSPVTEANTQYQQEASKLRQIRDTQ 120

Db 61 IVFSSGRGLYNSDVSKSTERYKKASDSSNTGVSSEANAQYQQEAAKLRQIGNLQ 120

Qy 121 NSNRHIVGESLGNFKELKNLEKIGISRVRSKKNELLVAEIEYMOKREMEIQHNNM 180

Db 121 NSNRHMLGEALSSLSVKELKSLEIRLEKGISRIRSKKNELLFAEIEYMOKREVDLHNNQ 180

Qy 181 YLRAKTAEGARLNPDOQESSVIOGTVYESGVSSHDQSHY-NRNYIPVNLLEPNQQFSG 239

Db 181 LLRAKISENER---KQSMNLMPPGADFET---VQSQPYDSRNYSQVNGLOPASHYSH 232

Qy 240 QDQPPQLQV 248

Db 233 QDQMALQLV 241

RESULT 9

AAG52721

ID AAG52721 standard; Protein; 300 AA.

XX AC AAG52721;

XX 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 67050.

DE Protein identification; signal transduction pathway; metabolic pathway;

XX hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.

XX Arabidopsis thaliana.

OS EP1033405-A2.

XX 06-SEP-2000.

PD 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 28-APR-1999; 99US-0130891.

PR 30-APR-1999; 99US-0131449.

PR 04-MAY-1999; 99US-0132048.

PR 05-MAY-1999; 99US-0132407.

PR 06-MAY-1999; 99US-0132484.

PR 06-MAY-1999; 99US-0132485.

PR 07-MAY-1999; 99US-0132486.

PR 11-MAY-1999; 99US-0132487.

PR 14-MAY-1999; 99US-0132863.

PR 14-MAY-1999; 99US-0134256.

PR 14-MAY-1999; 99US-0134218.

PR 14-MAY-1999; 99US-0134219.

PR 14-MAY-1999; 99US-0134221.

PR 18-MAY-1999; 99US-0134370.

PR 19-MAY-1999; 99US-0134768.

PR 20-MAY-1999; 99US-0134941.

PR 21-MAY-1999; 99US-0135124.

PR 24-MAY-1999; 99US-0135353.

PR 25-MAY-1999; 99US-0135629.

PR 27-MAY-1999; 99US-0136021.

PR 28-MAY-1999; 99US-0136392.

PR 01-JUN-1999; 99US-0136782.

PR 03-JUN-1999; 99US-0137222.

PR 04-JUN-1999; 99US-0137528.

PR 07-JUN-1999; 99US-0137724.

PR 08-JUN-1999; 99US-0138094.

PR 10-JUN-1999; 99US-0138540.

PR 14-JUN-1999; 99US-0138847.

PR 16-JUN-1999; 99US-0139119.

PR 17-JUN-1999; 99US-0139452.

PR 18-JUN-1999; 99US-0139453.

PR 18-JUN-1999; 99US-0139492.

PR 18-JUN-1999; 99US-0139454.

PR 18-JUN-1999; 99US-0139455.

PR 18-JUN-1999; 99US-0139456.

PR 18-JUN-1999; 99US-0139457.

PR 18-JUN-1999; 99US-0139458.

PR 18-JUN-1999; 99US-0139459.

PR 18-JUN-1999; 99US-0139460.

PR 18-JUN-1999; 99US-0139461.

PR 18-JUN-1999; 99US-0139462.

PR 18-JUN-1999; 99US-0139463.

PR 18-JUN-1999; 99US-0139750.

PR 21-JUN-1999; 99US-0139763.

PR 22-JUN-1999; 99US-0139817.

PR 23-JUN-1999; 99US-0139899.

PR 23-JUN-1999; 99US-0140353.

PR 24-JUN-1999; 99US-0140354.

PR 28-JUN-1999; 99US-0140695.

PR 29-JUN-1999; 99US-0140823.

PR 30-JUN-1999; 99US-0140991.

PR 01-JUL-1999; 99US-0141287.

PR 01-JUL-1999; 99US-0141842.

PR 02-JUL-1999; 99US-0142154.

PR 06-JUL-1999; 99US-0142055.

PR 06-JUL-1999; 99US-0142390.

PR 08-JUL-1999; 99US-0142803.

PR 09-JUL-1999; 99US-0142920.

PR 12-JUL-1999; 99US-0142377.

PR 13-JUL-1999; 99US-0143542.

PR 14-JUL-1999; 99US-0143624.

PR 15-JUL-1999; 99US-0144005.









CC and the desired protein is easily recovered from it. The recombinant  
CC proteins are useful for pharmaceutical purposes, as enzymes for biotests  
CC and antioxidants for food additives.

XX  
SQ Sequence 221 AA;  
  
Query Match 57.2%; Score 722; DB 21; Length 221;  
Best Local Similarity 64.7%; Pred. No. 9e-63;  
Matches 152; Conservative 30; Mismatches 37; Indels 16; Gaps 3;  
  
QY 16 LGRGKIEIKRIENTNRQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLYEYANN 75  
Db 1 MGRGKIEIKRIENTNRQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLYEYANN 60  
QY 76 SVRGTIERYKKACSDAVNPSPVTEANTQYQOEASKLRQIRDIQNSNRHIVGESLGS LN 135  
Db 61 SVKATIDRYKKASSDSNTGSTSEANTQFYQOEAAKLVRQIGNLQNSNRNMLGESLSLT 120  
QY 136 FKELKNLEGRLEKGISRVRSKKNELLVAETIYMQKREMELOHNNMYLRAKIAEGAR-LNP 194  
Db 121 AKDLKGLKETKLEKGISRSKKNELLFAETIYMRKREIDLHNNQMLRAKIAESERNVNM 180  
QY 195 DQESSVIQGTTVYESGVSSHDSQSOHYN-RNYIPVNLLEPNQOQSGDQPPQLQV 248  
Db 181 MGGEFELM-----QSHPYDPRDFQVNGLQHNHQPQDNMALQLV 221

RESULT 14  
AA58648  
ID AAY58648 standard; Protein; 221 AA.

XX AAY58648;

DT 11-APR-2000 (first entry)

DE Petunia nectary-specific FBp15 protein.

XX FBp14; nectary; nectar; transgenic plant; honey.

OS Petunia hybrida.

XX EP974667-A1.

XX 26-JAN-2000.

XX 16-JUL-1998; 98EP-0202375.

XX 16-JUL-1998; 98EP-0202375.

XX (CPRO-) CPRO-DLO CENT PLANTENVERDEDELINGS REPROD.

XX Creemers J, Angenent GC, Kater MM;

XX WPI; 2000-108400/10.

XX N-PSDB; AA235494.

PT Novel DNA sequences used to produce modified honey, the metabolites of  
PT which can be isolated and purified -

XX Claim 4; Page 26; 56pp; English.

CC The present sequence is that of Petunia hybrida strain W115 FBp15  
CC protein, a MADS box protein that is specifically expressed in the  
CC nectaries of petunia. The sequence was deduced from cDNA (see  
CC Z354940 identified by differential expression. The present  
CC invention provides a method for producing recombinant proteins in  
CC honey. The honey is manufactured by insects, preferably honeybees,  
CC that collect the nectar of transgenic plants. The FBp15 gene and  
CC its promoter can be utilised in expression cassettes for the  
CC production of transgenic plants that produce a protein of interest  
CC in their nectar.

XX Sequence 221 AA;

Query Match 57.2%; Score 722; DB 21; Length 221;  
Best Local Similarity 64.7%; Pred. No. 9e-63;  
Matches 152; Conservative 30; Mismatches 37; Indels 16; Gaps 3;  
  
QY 16 LGRGKIEIKRIENTNRQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLYEYANN 75  
Db 1 MGRGKIEIKRIENTNRQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLYEYANN 60  
QY 76 SVRGTIERYKKACSDAVNPSPVTEANTQYQOEASKLRQIRDIQNSNRHIVGESLGS LN 135  
Db 61 SVKATIDRYKKASSDSNTGSTSEANTQFYQOEAAKLVRQIGNLQNSNRNMLGESLSLT 120  
QY 136 FKELKNLEGRLEKGISRVRSKKNELLVAETIYMQKREMELOHNNMYLRAKIAEGAR-LNP 194  
Db 121 AKDLKGLKETKLEKGISRSKKNELLFAETIYMRKREIDLHNNQMLRAKIAESERNVNM 180  
QY 195 DQESSVIQGTTVYESGVSSHDSQSOHYN-RNYIPVNLLEPNQOQSGDQPPQLQV 248  
Db 181 MGGEFELM-----QSHPYDPRDFQVNGLQHNHQPQDNMALQLV 221

RESULT 15  
ABG60988

ID ABG60988 standard; Protein; 264 AA.

XX ABG60988;

XX 27-AUG-2002 (first entry)

XX Novel floral meristem identity protein LpMADS5.

XX Ryegrass; fescue; MADS-box; MADS; MADS-like protein; CENTRORADIALIS;  
KW CEN; CEN-like protein; APETALA2; AP2; AP2-like protein; HB;  
KW Homeo-box protein; HB-like protein; plant growth; plant architecture;  
KW inflorescence development; flower development; embryo development;  
KW seed development; flower organ identity; phase change; male sterility;  
KW hybrid seed production; herbage quality; early maturing crop;  
KW biomass increase; branching increase; blocking flowering;  
KW allergenic pollen; floral meristem identity protein.

OS Lolium perenne.

XX WO200233091-A1.

XX 25-APR-2002.

XX 17-OCT-2001; 2001WO-AU01311.

XX 19-OCT-2000; 2000AU-0000873.

XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
XX (AGRE-) AGRESEARCH LTD.

XX Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;

XX WPI; 2002-452388/48.

XX N-PSDB; ABR82132.

PT New substantially purified or isolated polypeptide e.g., MADS-box,  
PT CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or  
PT fescue species, useful for controlling plant life cycles and/or growth  
PT phases -

XX Claim 16; Fig 91; 290pp; English.

XX The invention describes a substantially purified or isolated polypeptide  
CC (I) from a ryegrass (Lolium sp.) or fescue (Festuca sp.) species, such as  
CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like  
CC proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)  
CC and HB-like proteins, or their functionally active fragments or variants.  
CC Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a  
CC vector (IV) comprising (II), is useful for modifying plant life cycles





GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2003, 12:42:28 ; Search time 26.1053 Seconds  
(without alignments)  
1957.448 Million cell updates/sec

Title: US-09-978-382A-4  
Perfect score: 1263  
Sequence: 1 MEEGGSSHDAESSKKLGRGK.....NLLEPNQFSGQDPPPLQLV 248

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_21.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match % | Length | DB ID     | Description        |
|------------|--------|---------------|--------|-----------|--------------------|
| 1          | 1170.5 | 92.7          | 249    | 10 Q9AXZ1 | Q9axz1 brassica na |
| 2          | 863    | 68.3          | 244    | 10 Q9XHM3 | Q9xhm3 liquidambar |
| 3          | 854    | 67.6          | 249    | 10 Q9MBE2 | Q9mbe2 rosa rugosa |
| 4          | 844    | 66.8          | 242    | 10 Q9BWD3 | Q8vwz3 malus domes |
| 5          | 837    | 66.3          | 225    | 10 Q93XH4 | Q93xh4 vitis vinif |
| 6          | 806    | 63.8          | 242    | 10 Q9LEP2 | Q9lep2 betula verr |
| 7          | 802    | 63.5          | 242    | 10 Q9ZTV9 | Q9ztv9 corylus ave |
| 8          | 797    | 63.1          | 247    | 10 Q40900 | Q40900 petunia int |
| 9          | 793    | 62.8          | 247    | 10 Q08711 | Q08711 petunia hyb |
| 10         | 781.5  | 61.9          | 239    | 10 Q41195 | Q41195 antirrhinum |
| 11         | 781    | 61.8          | 246    | 10 Q9ZS29 | Q9zs29 gerbera hyb |
| 12         | 780.5  | 61.8          | 246    | 10 Q9XFM8 | Q9xfm8 antirrhinum |
| 13         | 780.5  | 61.8          | 264    | 10 Q9ZS30 | Q9zs30 gerbera hyb |
| 14         | 769.5  | 60.9          | 241    | 10 Q65111 | Q65111 populus tri |
| 15         | 768    | 60.8          | 248    | 10 Q41352 | Q41352 silene lati |
| 16         | 766.5  | 60.7          | 239    | 10 Q8RVW5 | Q8rvw5 phalaenopsi |

|    |       |      |     |           |                    |
|----|-------|------|-----|-----------|--------------------|
| 17 | 764   | 60.5 | 245 | 10 Q8VWZ2 | Q8vwz2 malus domes |
| 18 | 763.5 | 60.5 | 248 | 10 Q9MBE1 | Q9mbe1 rosa rugosa |
| 19 | 762.5 | 60.4 | 248 | 10 Q9ZRH4 | Q9zrh4 rosa hybrid |
| 20 | 753   | 59.6 | 249 | 10 Q9MBE0 | Q9mbe0 rosa rugosa |
| 21 | 752.5 | 59.6 | 250 | 10 Q9MBD9 | Q9mbd9 rosa rugosa |
| 22 | 745.5 | 59.0 | 236 | 10 Q9ARE9 | Q9are9 cucumis sat |
| 23 | 740   | 58.6 | 244 | 10 Q8RVK1 | Q8rvk1 gossypium h |
| 24 | 739.5 | 58.6 | 228 | 10 Q9ZPK9 | Q9zpk9 hyacinthus  |
| 25 | 739.5 | 58.6 | 238 | 10 Q65112 | Q65112 populus tri |
| 26 | 729.5 | 57.8 | 253 | 10 Q42457 | Q42457 rumex aceto |
| 27 | 729   | 57.7 | 237 | 10 Q9SBK1 | Q9sbk1 cucumis sat |
| 28 | 729   | 57.7 | 249 | 10 Q9SBT4 | Q9sbt4 fragaria an |
| 29 | 729   | 57.7 | 262 | 10 Q64958 | Q64958 cucumis sat |
| 30 | 717   | 56.8 | 225 | 10 Q9SBK3 | Q9sbk3 cucumis sat |
| 31 | 705   | 55.8 | 221 | 10 Q9LKQ1 | Q9lkg1 cucumis sat |
| 32 | 705   | 55.8 | 229 | 10 Q64959 | Q64959 cucumis sat |
| 33 | 698.5 | 55.3 | 236 | 10 Q40704 | Q40704 oryza sativ |
| 34 | 698.5 | 55.3 | 247 | 10 Q9AWJ2 | Q9awj2 oryza sativ |
| 35 | 695.5 | 55.1 | 254 | 10 Q43422 | Q43422 cucumis sat |
| 36 | 693   | 54.9 | 234 | 10 Q8RU44 | Q8ru44 hordeum vul |
| 37 | 692   | 54.8 | 254 | 10 Q9SBK2 | Q9sbk2 cucumis sat |
| 38 | 689   | 54.6 | 215 | 10 Q93XE3 | Q93xe3 cucumis sat |
| 39 | 682   | 54.0 | 208 | 10 Q948V3 | Q948v3 magnolia pr |
| 40 | 679   | 53.8 | 232 | 10 Q8RU43 | Q8ru43 hordeum vul |
| 41 | 676.5 | 53.6 | 228 | 10 Q40882 | Q40882 petunia hyb |
| 42 | 670   | 53.0 | 259 | 10 Q24009 | Q24009 zea mays (m |
| 43 | 653.5 | 51.7 | 222 | 10 Q9ZTY6 | Q9ztv6 pinus resin |
| 44 | 651.5 | 51.6 | 222 | 10 Q9ZTW4 | Q9ztw4 pinus radia |
| 45 | 649.5 | 51.4 | 222 | 10 Q9ZRC6 | Q9zrc6 picea maria |

## ALIGNMENTS

## RESULT 1

|        |                                                                       |        |              |      |         |
|--------|-----------------------------------------------------------------------|--------|--------------|------|---------|
| Q9AXZ1 | ID                                                                    | Q9AXZ1 | PRELIMINARY; | PRT; | 249 AA. |
| AC     | Q9AXZ1;                                                               |        |              |      |         |
| DT     | 01-JUN-2001 (Tremblrel. 17, Created)                                  |        |              |      |         |
| DT     | 01-JUN-2001 (Tremblrel. 17, Last sequence update)                     |        |              |      |         |
| DT     | 01-MAR-2002 (Tremblrel. 20, Last annotation update)                   |        |              |      |         |
| DE     | SHATTERPROOF1.                                                        |        |              |      |         |
| GN     | BNSHP1.                                                               |        |              |      |         |
| OS     | Brassica napus (Rape).                                                |        |              |      |         |
| OC     | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;    |        |              |      |         |
| OC     | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; |        |              |      |         |
| OC     | eurosid II; Brassicales; Brassicaceae; Brassica.                      |        |              |      |         |
| OX     | NCBI_TaxID=3708;                                                      |        |              |      |         |
| RN     | [1]                                                                   |        |              |      |         |
| RP     | SEQUENCE FROM N.A.                                                    |        |              |      |         |
| RC     | STRAIN=CV. BRIDGER;                                                   |        |              |      |         |
| RA     | Pylatuik J.D., Davis A.R., Bonham-Smith P.C.;                         |        |              |      |         |
| RT     | "Molecular cloning and characterization of a B. napus SHP1 gene.";    |        |              |      |         |
| RL     | Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.               |        |              |      |         |
| RN     | [2]                                                                   |        |              |      |         |
| RP     | SEQUENCE FROM N.A.                                                    |        |              |      |         |
| RA     | Pylatuik J.D., Davis A.R., Bonham-Smith P.C.;                         |        |              |      |         |
| RT     | "Isolation of the coding region of BnSHP by RT-PCR.";                 |        |              |      |         |
| RL     | Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.               |        |              |      |         |
| CC     | -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).                    |        |              |      |         |
| CC     | -!- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.   |        |              |      |         |
| DR     | EMBL; AF226865; AAK00646.1; -                                         |        |              |      |         |
| DR     | EMBL; AY036062; AAK62033.1; -                                         |        |              |      |         |
| DR     | HSSP; P11746; 1MNM.                                                   |        |              |      |         |
| DR     | InterPro; IPR002487; TF_Kbox.                                         |        |              |      |         |
| DR     | InterPro; IPR002100; TF_MADSbox.                                      |        |              |      |         |
| DR     | Pfam; PF01486; K-box; 1.                                              |        |              |      |         |
| DR     | Pfam; PF00319; SRF-TF; 1.                                             |        |              |      |         |
| DR     | PRINTS; PR00404; MADSDOMAIN.                                          |        |              |      |         |
| DR     | SMART; SM00432; MADS; 1.                                              |        |              |      |         |
| DR     | PROSITE; PS00350; MADS_BOX_1; 1.                                      |        |              |      |         |
| DR     | PROSITE; PS0066; MADS_BOX_2; 1.                                       |        |              |      |         |
| KW     | DNA-binding; Nuclear protein; Transcription regulation.               |        |              |      |         |

|          |                                                                     |                                                               |                    |                         |             |
|----------|---------------------------------------------------------------------|---------------------------------------------------------------|--------------------|-------------------------|-------------|
| SQ       | SEQUENCE                                                            | 249 AA;                                                       | 28219 MW;          | BE78E063E1F5FB4E CRC64; |             |
|          | Query Match                                                         | 92.7%;                                                        | Score 1170.5;      | DB 10;                  | Length 249; |
|          | Best Local Similarity                                               | 92.4%;                                                        | Pred. No. 5.9e-75; |                         |             |
|          | Matches                                                             | 230;                                                          | Conservative 11;   | Mismatches 7;           | Indels 1;   |
|          | Gaps                                                                | 1;                                                            |                    |                         |             |
| QY       | 1                                                                   | MEEGSSHDAESSKKLGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVAL   | 60                 |                         |             |
| DB       | 1                                                                   | MDEGSSHDAESSKKIGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVAL   | 60                 |                         |             |
| QY       | 61                                                                  | VIFSTRGRLEYANNVSRGTIERYKKACSDAVNPPSVTEANTQYYQQEASKLRRIQDIQ    | 120                |                         |             |
| DB       | 61                                                                  | VIFSTRGLLEYASNSVKGTIERYKKACSDAVNPPTVTEANTKHYYQQEASKLRRIQDIQ   | 120                |                         |             |
| QY       | 121                                                                 | NSNRHIVGESLGSINFKELKNLEGRLEKGISRVSKKNELLVAEIEYMQKREMELOHNNM   | 180                |                         |             |
| DB       | 121                                                                 | NSNRHIVGESLGSINFKELKNLEGRLEKGISRVSKKSELLVAEIEYMQKREMELOHNNM   | 180                |                         |             |
| QY       | 181                                                                 | YLRAKIAEGARLNPDOQESSVIOGTTVYESGV-SSHDQSOHYNRYNIPVNLLEPNQOQFSG | 239                |                         |             |
| DB       | 181                                                                 | YLRAKIEQGARLNPQHGSGVIOGTTAVYESGLSSHDQSOHYNRYNIPVNLLEPNQOQFSG  | 240                |                         |             |
| QY       | 240                                                                 | QDQPPLQLV 248                                                 |                    |                         |             |
| DB       | 241                                                                 | QDQPPLQLV 249                                                 |                    |                         |             |
| RESULT 2 |                                                                     |                                                               |                    |                         |             |
| Q9XHM3   |                                                                     | PRELIMINARY;                                                  | PRT;               | 244 AA.                 |             |
| ID       | Q9XHM3                                                              |                                                               |                    |                         |             |
| AC       | Q9XHM3;                                                             |                                                               |                    |                         |             |
| DT       | 01-NOV-1999 (TREMBlrel. 12, Created)                                |                                                               |                    |                         |             |
| DT       | 01-NOV-1999 (TREMBlrel. 12, Last sequence update)                   |                                                               |                    |                         |             |
| DT       | 01-MAR-2002 (TREMBlrel. 20, Last annotation update)                 |                                                               |                    |                         |             |
| DE       | Agamous homolog (Fragment).                                         |                                                               |                    |                         |             |
| GN       | LAG.                                                                |                                                               |                    |                         |             |
| OS       | Liquidambar styraciflua (Amberboom) (Sweetgum tree).                |                                                               |                    |                         |             |
| OC       | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  |                                                               |                    |                         |             |
| OC       | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;        |                                                               |                    |                         |             |
| OC       | Saxifragales; Hamamelidaceae; Liquidambar.                          |                                                               |                    |                         |             |
| OX       | NCBI_TaxID=4400;                                                    |                                                               |                    |                         |             |
| RN       | [1]                                                                 |                                                               |                    |                         |             |
| RP       | SEQUENCE FROM N.A.                                                  |                                                               |                    |                         |             |
| RA       | Liu J., Huang Y., Ding B., Tauer C.G.;                              |                                                               |                    |                         |             |
| RT       | "cDNA cloning and expression of a sweetgum gene that shows homology |                                                               |                    |                         |             |
| RT       | with Arabidopsis AGAMOUS."                                          |                                                               |                    |                         |             |
| RL       | Plant Sci. 142:73-82(1999).                                         |                                                               |                    |                         |             |
| CC       | - - SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).                  |                                                               |                    |                         |             |
| CC       | - - SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS. |                                                               |                    |                         |             |
| DR       | EMBL; AF103903; AAD38119.1; -.                                      |                                                               |                    |                         |             |
| DR       | HSSP; P11746; 1NMN.                                                 |                                                               |                    |                         |             |
| DR       | InterPro; IPR002487; TF_Kbox.                                       |                                                               |                    |                         |             |
| DR       | InterPro; IPR002100; TF_MADSbox.                                    |                                                               |                    |                         |             |
| DR       | Pfam; PF01486; K-box; 1.                                            |                                                               |                    |                         |             |
| DR       | Pfam; PF00319; SRF-TF; 1.                                           |                                                               |                    |                         |             |
| DR       | PRINTS; PR00404; MADSDOMAIN.                                        |                                                               |                    |                         |             |
| DR       | SMART; SM00432; MADS; 1.                                            |                                                               |                    |                         |             |
| DR       | PROSITE; PS00350; MADS_BOX_1; 1.                                    |                                                               |                    |                         |             |
| DR       | PROSITE; PS50066; MADS_BOX_2; 1.                                    |                                                               |                    |                         |             |
| KW       | DNA-binding; Nuclear protein; Transcription regulation.             |                                                               |                    |                         |             |
| FT       | NON_TER 1                                                           |                                                               |                    |                         |             |
| SQ       | SEQUENCE 244 AA; 28205 MW; A7BF0F928D52EAA8 CRC64;                  |                                                               |                    |                         |             |
|          | Query Match                                                         | 68.3%;                                                        | Score 863;         | DB 10;                  | Length 244; |
|          | Best Local Similarity                                               | 73.0%;                                                        | Pred. No. 2.5e-53; |                         |             |
|          | Matches                                                             | 178;                                                          | Conservative 28;   | Mismatches 28;          | Indels 10;  |
|          | Gaps                                                                | 5;                                                            |                    |                         |             |
| QY       | 6                                                                   | SSHDAESSKKLGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVALVFST   | 65                 |                         |             |
| DB       | 10                                                                  | SEGGSSQKKMGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEIALVFSS      | 69                 |                         |             |
| QY       | 66                                                                  | RGRLEYANNVSRGTIERYKKACSDAVNPPSVTEANTQYYQQEASKLRRIQDIQNSNRH    | 125                |                         |             |

|          |                                                                       |                                                               |                    |                |             |
|----------|-----------------------------------------------------------------------|---------------------------------------------------------------|--------------------|----------------|-------------|
| Db       | 70                                                                    | RGRLEYANNVSKSTIERYKKA-SDTSNPGSVSETNAQFYQQESSKLRRIQDIQNLNRH    | 128                |                |             |
| QY       | 126                                                                   | IVGESLGSINFKELKNLEGRLEKGISRVSKKNELLVAEIEYMQKREMELOHNNMYLRAK   | 185                |                |             |
| DB       | 129                                                                   | IMGEALSSLTFRLEKNLEGRLEKGISRIRSKKNELLFAEIEYMQKRETELQANMYLRAK   | 188                |                |             |
| QY       | 186                                                                   | IAGCARLNPDOQESSVIOGTTVYESGVSSHDSOHOYHNRNYPVNLLE-PNQOFSGODQPP  | 244                |                |             |
| DB       | 189                                                                   | IAENER---NQOQTELMFG-SVYETMPS----SQPYDRSFLVANLLEPPNHHYSRODQTP  | 240                |                |             |
| QY       | 245                                                                   | LQLV 248                                                      |                    |                |             |
| DB       | 241                                                                   | LQLV 244                                                      |                    |                |             |
| RESULT 3 |                                                                       |                                                               |                    |                |             |
| Q9MBE2   |                                                                       | PRELIMINARY;                                                  | PRT;               | 249 AA.        |             |
| ID       | Q9MBE2                                                                |                                                               |                    |                |             |
| AC       | Q9MBE2;                                                               |                                                               |                    |                |             |
| DT       | 01-OCT-2000 (TREMBlrel. 15, Created)                                  |                                                               |                    |                |             |
| DT       | 01-OCT-2000 (TREMBlrel. 15, Last sequence update)                     |                                                               |                    |                |             |
| DT       | 01-MAR-2002 (TREMBlrel. 20, Last annotation update)                   |                                                               |                    |                |             |
| DE       | MADS-box protein.                                                     |                                                               |                    |                |             |
| GN       | MASAKO D1.                                                            |                                                               |                    |                |             |
| OS       | Rosa rugosa (Rugosa rose).                                            |                                                               |                    |                |             |
| OC       | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;    |                                                               |                    |                |             |
| OC       | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; |                                                               |                    |                |             |
| OC       | eurosid I; Rosales; Rosaceae; Rosoideae; Rosa.                        |                                                               |                    |                |             |
| OX       | NCBI_TaxID=74645;                                                     |                                                               |                    |                |             |
| RN       | [1]                                                                   |                                                               |                    |                |             |
| RP       | SEQUENCE FROM N.A.                                                    |                                                               |                    |                |             |
| RC       | TISSUE=FLOWER;                                                        |                                                               |                    |                |             |
| RX       | PubMed=10808068;                                                      |                                                               |                    |                |             |
| RA       | Kitahara K., Matsumoto S.;                                            |                                                               |                    |                |             |
| RT       | "Rose MADS-box genes 'MASAKO C1 and D1' homologous to class C floral  |                                                               |                    |                |             |
| RT       | identity genes."                                                      |                                                               |                    |                |             |
| RL       | Plant Sci. 151:121-134(2000).                                         |                                                               |                    |                |             |
| CC       | - - SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).                    |                                                               |                    |                |             |
| CC       | - - SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.   |                                                               |                    |                |             |
| DR       | EMBL; AB025643; BAA90743.1; -.                                        |                                                               |                    |                |             |
| DR       | HSSP; P11746; 1NMN.                                                   |                                                               |                    |                |             |
| DR       | InterPro; IPR002487; TF_Kbox.                                         |                                                               |                    |                |             |
| DR       | InterPro; IPR002100; TF_MADSbox.                                      |                                                               |                    |                |             |
| DR       | Pfam; PF01486; K-box; 1.                                              |                                                               |                    |                |             |
| DR       | Pfam; PF00319; SRF-TF; 1.                                             |                                                               |                    |                |             |
| DR       | PRINTS; PR00404; MADSDOMAIN.                                          |                                                               |                    |                |             |
| DR       | SMART; SM00432; MADS; 1.                                              |                                                               |                    |                |             |
| DR       | PROSITE; PS00350; MADS_BOX_1; 1.                                      |                                                               |                    |                |             |
| DR       | PROSITE; PS50066; MADS_BOX_2; 1.                                      |                                                               |                    |                |             |
| KW       | DNA-binding; Nuclear protein; Transcription regulation.               |                                                               |                    |                |             |
| SQ       | SEQUENCE 249 AA; 28796 MW; 16F5AC7857C17803 CRC64;                    |                                                               |                    |                |             |
|          | Query Match                                                           | 67.6%;                                                        | Score 854;         | DB 10;         | Length 249; |
|          | Best Local Similarity                                                 | 71.5%;                                                        | Pred. NO. 1.1e-52; |                |             |
|          | Matches                                                               | 176;                                                          | Conservative 32;   | Mismatches 22; | Indels 16;  |
|          | Gaps                                                                  | 6;                                                            |                    |                |             |
| QY       | 9                                                                     | DAESSKKLGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVALVFSTRGR   | 68                 |                |             |
| DB       | 14                                                                    | ESSQKKLGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVALVFSTRGR    | 73                 |                |             |
| QY       | 69                                                                    | LYEYANNVSRGTIERYKKACSDAVNPPSVTEANTQYYQQEASKLRRIQDIQNSNRHIVG   | 128                |                |             |
| DB       | 74                                                                    | LYEYANNVSRGTIERYKKAC-DSSNTGTSVTETNVQFYQQEASKLRRIQDIQNSNRHILG  | 132                |                |             |
| QY       | 129                                                                   | ESLGSINFKELKNLEGRLEKGISRVSKKNELLVAEIEYMQKREMELOHNNMYLRAKIAE   | 188                |                |             |
| DB       | 133                                                                   | EALSTLNVKELKNLEGRLEKGISRIRSKKNEMLFAEIEYMQKRETELQNNFLRAKIAE    | 192                |                |             |
| QY       | 189                                                                   | GARLNPDOQESSVIOGTTVYESGVSSHDSQ-----QHYNRYNIPVNLLEPNQOFS--GQDQ | 242                |                |             |
| DB       | 193                                                                   | NDR--AQOQANMMFCT-----LSAYDQSMPPQSYDRSFLPV-ILESNNHHYNRQGNQ     | 243                |                |             |
| QY       | 243                                                                   | PPLQLV 248                                                    |                    |                |             |



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DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00350; MADS_BOX_2; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 242 AA; 27977 MW; CE112695AEDC5ED6 CRC64;

Query Match      63.8%; Score 806; DB 10; Length 242;
Best Local Similarity 67.2%; Pred. No. 2.5e-49;
Matches 168; Conservative 28; Mismatches 44; Indels 10; Gaps 4;

QY 1 MEEGSSHDAESSKLGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVAL 60
DB 1 MEFQNSMSVSPQKLGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEIAL 60

QY 61 VIFSTRGRLYEYANN-SVRGTIERYYKACSDAVNPPSVTEANTQYYQOEASKLRQIRDI 119
DB 61 IVFSSRGRLYEYANNSSVKTIERYKKACADSSSGSVSEANTQFYQOEAAKLRGQIRSV 120

QY 120 QNSNRHIVGESLGNFKELNLEKLGISRVRSKKNELLVAEIEYMQKREMELOHNN 179
DB 121 QDSNRHMLGEALSELNFKELNLEKLGINIRSKKNELLVAEIEYMHKREVDLHNNN 180

QY 180 MYLRAKIAEAGARLNPDQESSVIQGTTVYESGVSHDQSOHY-NRNYIPVNLLEPNQQFS 238
DB 181 QILRAKIAENER---NQNLNVMPPGGNYEL-----MQSQSDSRNYFQVDALQPNHHYP 232

QY 239 GDQPPPLQLV 248
DB 233 RQDOIPQLV 242

RESULT 7
Q9ZTV9 ID Q9ZTV9 PRELIMINARY; PRT; 242 AA.
AC Q9ZTV9;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE MADS1.
GN MADS1.
OS Corylus avellana (European hazel).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC eurosids I; Fagales; Betulaceae; Corylus.
OX NCBI_TaxID=13451;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99084765; PubMed=9869420;
RA Rigola D., Pe M.E., Fabrizio C., Me G., Sari-Gorla M.;
RT "CaMADS1, a MADS box gene expressed in the carpel of hazelnut.";
RL Plant Mol. Biol. 38:1147-1160(1998).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL; AF027376; AAD03486.1; -.
DR HSSP; P11746; 1MNM.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 2.
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 242 AA; 28023 MW; 6D74CD8654A1B719 CRC64;

Query Match      63.5%; Score 802; DB 10; Length 242;
Best Local Similarity 66.4%; Pred. No. 4.8e-49;
Matches 166; Conservative 31; Mismatches 43; Indels 10; Gaps 4;
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QY 1 MEEGSSHDAESSKLGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVAL 60
DB 1 MEFQNSMSVSPQKLGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEIAL 60

QY 61 VIFSTRGRLYEYANN-SVRGTIERYYKACSDAVNPPSVTEANTQYYQOEASKLRQIRDI 119
DB 61 IVFSSRGRLYEYANNSSVKTIERYKKACADSSSGSVSEANTQFYQOEAAKLRGQIRSV 120

QY 120 QNSNRHIVGESLGNFKELNLEKLGISRVRSKKNELLVAEIEYMQKREMELOHNN 179
DB 121 QDSNRHMLGEALSELNFKELNLEKLGINIRSKKNELLVAEIEYMHKREVDLHNNN 180

QY 180 MYLRAKIAEAGARLNPDQESSVIQGTTVYESGVSHDQSOHY-NRNYIPVNLLEPNQQFS 238
DB 181 QILRAKIAENER---NQNLNVMPPGGNYEL-----MQSQSDSRNYFQVDALQPNHHYP 232

QY 239 GDQPPPLQLV 248
DB 233 RQDOIPQLV 242

RESULT 8
Q40900 ID Q40900 PRELIMINARY; PRT; 247 AA.
AC Q40900;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Agamous protein.
GN PAGL1.
OS Petunia integrifolia (Violet-flowered petunia) (Petunia inflata).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
OX NCBI_TaxID=4103;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PISTIL;
RA Karunanandaa B., Kao T.-h.;
RT "Characterization of a flower-specific cDNA of Petunia inflata
RT encoding a putative homolog of Agamous protein.";
RL Submitted (JUN-1995) to the EMBL/GenBank/DBDJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL; L33973; AAA68001.1; -.
DR HSSP; P11746; 1MNM.
DR TRANSFAC; T03126; -.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 247 AA; 28389 MW; C1A5F1F0B6E9BECF CRC64;

Query Match      63.1%; Score 797; DB 10; Length 247;
Best Local Similarity 68.6%; Pred. No. 1.1e-48;
Matches 164; Conservative 28; Mismatches 45; Indels 2; Gaps 1;

QY 10 AESSKLGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGRL 69
DB 11 SSSQKSGRGRKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSSRGR 70

QY 70 YEVANNSVRGTIERYYKACSDAVNPPSVTEANTQYYQOEASKLRQIRDIQNSNRHIVGE 129
DB 71 YEVANNSVRATIDRYKKHHADSTSTGVSSEANTQYYQOEAAKLRQIRDIQTNRQIVGE 130

QY 130 SLGSLNFKELNLEKLGISRVRSKKNELLVAEIEYMQKREMELOHNNMYLRAKIAEG 189
DB 131 SLGSLNFKELNLEKLGISRVRSKKNELLVAEIEYMQKREMELOHNNMYLRAKIAEG 189
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|                                                             |                                                                     |                                                               |              |
|-------------------------------------------------------------|---------------------------------------------------------------------|---------------------------------------------------------------|--------------|
| Db                                                          | 131                                                                 | ALSSLSPRDLKNLEGLKKAIGVRVRKKNKLLFSEITLMQKREIEMQNANMYLRAKIAEV   | 190          |
| Qy                                                          | 190                                                                 | ARLNPDOQESSVIQGTTVYESGVSHDQSOHYNNRNYIPVNLLPEPNQOQSGODOPPLQLV  | 248          |
| Db                                                          | 191                                                                 | ERAT--QQMNLMPGGGSEYQQQPMSSSTSQPYDARNFLPVNLLPEPNPHYSRODOTALQLV | 247          |
| RESULT 9                                                    |                                                                     |                                                               |              |
| Q08711                                                      |                                                                     | PRELIMINARY;                                                  | PRT; 247 AA. |
| ID                                                          | Q08711                                                              |                                                               |              |
| AC                                                          | Q08711;                                                             |                                                               |              |
| DT                                                          | 01-NOV-1996 (Tremblrel. 01, Created)                                |                                                               |              |
| DT                                                          | 01-NOV-1996 (Tremblrel. 01, Last sequence update)                   |                                                               |              |
| DT                                                          | 01-MAR-2002 (Tremblrel. 20, Last annotation update)                 |                                                               |              |
| DE                                                          | Fbp6 protein.                                                       |                                                               |              |
| GN                                                          | FBP6.                                                               |                                                               |              |
| OS                                                          | Petunia hybrida (Petunia).                                          |                                                               |              |
| OC                                                          | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  |                                                               |              |
| OC                                                          | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;        |                                                               |              |
| OC                                                          | Asteridae; euasterids I; Solanales; Solanaceae; Petunia.            |                                                               |              |
| OX                                                          | NCBI_TaxID=4102;                                                    |                                                               |              |
| RN                                                          | [1]                                                                 |                                                               |              |
| RC                                                          | SEQUENCE FROM N.A.                                                  |                                                               |              |
| RC                                                          | STRAIN=W115; TISSUE=CARPEL;                                         |                                                               |              |
| RA                                                          | Luw J.B.;                                                           |                                                               |              |
| RL                                                          | Submitted (OCT-1992) to the EMBL/GenBank/DBRJ databases.            |                                                               |              |
| RL                                                          | [2]                                                                 |                                                               |              |
| RN                                                          | SEQUENCE FROM N.A.                                                  |                                                               |              |
| RC                                                          | STRAIN=W115; TISSUE=CARPEL;                                         |                                                               |              |
| RC                                                          | MEDLINE=94035167; PubMed=8106081;                                   |                                                               |              |
| RA                                                          | Angenent G.C., Franken J., Busscher M., Colombo L., van Tunen A.J.; |                                                               |              |
| RT                                                          | "Petal and stamen formation in petunia is regulated by the homeotic |                                                               |              |
| RT                                                          | gene fbpl.";                                                        |                                                               |              |
| RT                                                          | Plant J. 4:101-112(1993).                                           |                                                               |              |
| CC                                                          | -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).                  |                                                               |              |
| CC                                                          | -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS. |                                                               |              |
| DR                                                          | EMBL; X68675; CAA48635.1; -.                                        |                                                               |              |
| DR                                                          | HSSP; P11746; 1NMN.                                                 |                                                               |              |
| DR                                                          | TRANSEAC; T03094; -.                                                |                                                               |              |
| DR                                                          | InterPro; IPR002487; TF_Kbox.                                       |                                                               |              |
| DR                                                          | InterPro; IPR002100; TF_MADSbox.                                    |                                                               |              |
| DR                                                          | Pfam; PF01486; K-box; 1.                                            |                                                               |              |
| DR                                                          | Pfam; PF00319; SRP-TF; 1.                                           |                                                               |              |
| DR                                                          | PRINTS; PR00404; MADSDOMAIN.                                        |                                                               |              |
| DR                                                          | SMART; SM00432; MADS; 1.                                            |                                                               |              |
| DR                                                          | PROSITE; PS00350; MADS_BOX_1; 1.                                    |                                                               |              |
| DR                                                          | PROSITE; PS00066; MADS_BOX_2; 1.                                    |                                                               |              |
| KW                                                          | DNA-binding; Nuclear protein; Transcription regulation.             |                                                               |              |
| SQ                                                          | SEQUENCE 247 AA; 28371 MW; 31B7A8D425199DA2 CRC64;                  |                                                               |              |
| Query Match 62.8%; Score 793; DB 10; Length 247;            |                                                                     |                                                               |              |
| Best Local Similarity 68.6%; Pred. No. 2.1e-48;             |                                                                     |                                                               |              |
| Matches 164; Conservative 27; Mismatches 46; Indels 2; Gaps |                                                                     |                                                               |              |
| Qy                                                          | 10                                                                  | AESSKILGRGKTEIKRIENTTNRQVTCRRNGLLKKAYELSVLCDAEVALVIFSTRGL     | 69           |
| Db                                                          | 11                                                                  | SSSQKSGRGKTEIKRIENTTNRQVTCRRNGLLKKAYELSVLCDAEVALVIFSSRGL      | 70           |
| Qy                                                          | 70                                                                  | YEYANNSVRGTIERYKKACSDAVNPPSVTEANTQYQOEAKLRQRIRDIQNSNRHIVGE    | 129          |
| Db                                                          | 71                                                                  | YEYANNSVRATIDRYKKHHADSTSGVSEANTQYQOEAAKLRRQIRDIQYNRQIVGE      | 130          |
| Qy                                                          | 130                                                                 | SLGSLNFKELKLEGRLEKIGISVRSKKNLELLVAEITYMQKREMELOHNNMYLRAKIAEG  | 189          |
| Db                                                          | 131                                                                 | ALSSLSPRGLKNLEGLKKAIGVRVRKKNKLLFSEITLMQKREIEMQNANMYLRAKIAEV   | 190          |
| Qy                                                          | 190                                                                 | ARLNPDOQESSVIQGTTVYESGVSHDQSOHYNNRNYIPVNLLPEPNQOQSGODOPPLQLV  | 248          |
| Db                                                          | 191                                                                 | ERAT--QQMNLMPGGGSEYQQQPMSSSTSQPYDARNFLPVNLLPEPNPHYSRODOTALQLV | 247          |
| RESULT 10                                                   |                                                                     |                                                               |              |
| Q41195                                                      |                                                                     |                                                               |              |



|                                                                                                                   |                                                                       |                                                              |     |  |  |  |  |  |  |
|-------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------|--------------------------------------------------------------|-----|--|--|--|--|--|--|
| Best Local Similarity 64.8%; Pred. No. 1.7e-47;<br>Matches 158; Conservative 33; Mismatches 44; Indels 9; Gaps 4; |                                                                       |                                                              |     |  |  |  |  |  |  |
| QY                                                                                                                | 9                                                                     | DAESSKLGKGIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGR      | 68  |  |  |  |  |  |  |
| Db                                                                                                                | 26                                                                    | DMSQPKMGKGIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSSRGR      | 85  |  |  |  |  |  |  |
| QY                                                                                                                | 69                                                                    | LYEYANNSVGRGTIERYKKACSDAVNPPSVTEANTQYQOEASKLRRIQDQNSN- - - R | 124 |  |  |  |  |  |  |
| Db                                                                                                                | 86                                                                    | LYEYANNSVGTIDYKKACLDPTSGTVAEANTQYQOEAAKLQQIANLQNRQFYR        | 145 |  |  |  |  |  |  |
| QY                                                                                                                | 125                                                                   | HIVGESLGNFKELNLEGRLEKIGISVRSKKNELLVAEIEYMQKREMELOHNNMYLRA    | 184 |  |  |  |  |  |  |
| Db                                                                                                                | 146                                                                   | NIMGESLGMVVDLKNLEGLKEAISIRAKKNELLFAEIEYMQKRELEHNSNQFLRA      | 205 |  |  |  |  |  |  |
| QY                                                                                                                | 185                                                                   | KIABGARLNPDOQESSVIQTTVYESGVSSHDSQSHYNNRYIPVNLLEPNQOFSGQDQPP  | 244 |  |  |  |  |  |  |
| Db                                                                                                                | 206                                                                   | KIVENER- -AQHHMSLMPGSSDYEL-VTPHQPF- -GRNYLQTNLQPNNDYSCQDQTP  | 260 |  |  |  |  |  |  |
| QY                                                                                                                | 245                                                                   | LQLV 248                                                     |     |  |  |  |  |  |  |
| Db                                                                                                                | 261                                                                   | LQLV 264                                                     |     |  |  |  |  |  |  |
| RESULT 14                                                                                                         |                                                                       |                                                              |     |  |  |  |  |  |  |
| O65111                                                                                                            |                                                                       |                                                              |     |  |  |  |  |  |  |
| ID                                                                                                                | O65111                                                                | PRELIMINARY; PRT; 241 AA.                                    |     |  |  |  |  |  |  |
| AC                                                                                                                | O65111;                                                               |                                                              |     |  |  |  |  |  |  |
| DT                                                                                                                | 01-AUG-1998 (TREMBLrel. 07, Created)                                  |                                                              |     |  |  |  |  |  |  |
| DT                                                                                                                | 01-AUG-1998 (TREMBLrel. 07, Last sequence update)                     |                                                              |     |  |  |  |  |  |  |
| DE                                                                                                                | 01-MAR-2002 (TREMBLrel. 20, Last annotation update)                   |                                                              |     |  |  |  |  |  |  |
| DE                                                                                                                | Agamous homolog.                                                      |                                                              |     |  |  |  |  |  |  |
| GN                                                                                                                | PTAG1.                                                                |                                                              |     |  |  |  |  |  |  |
| OS                                                                                                                | Populus trichocarpa (Western balsam poplar).                          |                                                              |     |  |  |  |  |  |  |
| OC                                                                                                                | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;    |                                                              |     |  |  |  |  |  |  |
| OC                                                                                                                | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; |                                                              |     |  |  |  |  |  |  |
| OC                                                                                                                | eurosids I; Malpighiales; Salicaceae; Populus.                        |                                                              |     |  |  |  |  |  |  |
| OX                                                                                                                | NCBI_TaxID=3694;                                                      |                                                              |     |  |  |  |  |  |  |
| RN                                                                                                                | [1]                                                                   |                                                              |     |  |  |  |  |  |  |
| RP                                                                                                                | SEQUENCE FROM N.A.                                                    |                                                              |     |  |  |  |  |  |  |
| RA                                                                                                                | Brunner A.M., Rottmann W.H., Sheppard L.A., Strauss S.H.;             |                                                              |     |  |  |  |  |  |  |
| RT                                                                                                                | "Two Populus trichocarpa genes homologous to AGAMOUS.;"               |                                                              |     |  |  |  |  |  |  |
| RL                                                                                                                | Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.               |                                                              |     |  |  |  |  |  |  |
| CC                                                                                                                | -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).                    |                                                              |     |  |  |  |  |  |  |
| CC                                                                                                                | -!- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.   |                                                              |     |  |  |  |  |  |  |
| DR                                                                                                                | EMBL; AF052570; AAC06237.1; -.                                        |                                                              |     |  |  |  |  |  |  |
| DR                                                                                                                | HSSP; P11746; 1MNN.                                                   |                                                              |     |  |  |  |  |  |  |
| DR                                                                                                                | InterPro; IPR002487; TF_Kbox.                                         |                                                              |     |  |  |  |  |  |  |
| DR                                                                                                                | InterPro; IPR002100; TF_MADSbox.                                      |                                                              |     |  |  |  |  |  |  |
| DR                                                                                                                | Pfam; PF01486; K-box; 1.                                              |                                                              |     |  |  |  |  |  |  |
| DR                                                                                                                | Pfam; PF00319; SRF-TF; 1.                                             |                                                              |     |  |  |  |  |  |  |
| DR                                                                                                                | PRINTS; PR00404; MADSDOMAIN.                                          |                                                              |     |  |  |  |  |  |  |
| DR                                                                                                                | SMART; SM00432; MADS; 1.                                              |                                                              |     |  |  |  |  |  |  |
| DR                                                                                                                | PROSITE; PS00350; MADS_BOX_1; 1.                                      |                                                              |     |  |  |  |  |  |  |
| DR                                                                                                                | PROSITE; PS50066; MADS_BOX_2; 1.                                      |                                                              |     |  |  |  |  |  |  |
| KW                                                                                                                | DNA-binding; Nuclear protein; Transcription regulation.               |                                                              |     |  |  |  |  |  |  |
| SQ                                                                                                                | SEQUENCE 241 AA; 27559 MW; 4C2BFD11F29E99CF CRC64;                    |                                                              |     |  |  |  |  |  |  |
| Query Match 60.9%; Score 769.5; DB 10; Length 241;                                                                |                                                                       |                                                              |     |  |  |  |  |  |  |
| Best Local Similarity 64.7%; Pred. No. 9.2e-47;                                                                   |                                                                       |                                                              |     |  |  |  |  |  |  |
| Matches 161; Conservative 35; Mismatches 44; Indels 9; Gaps 3;                                                    |                                                                       |                                                              |     |  |  |  |  |  |  |
| QY                                                                                                                | 1                                                                     | MEEGSSHDABSSKLGKGIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVAL       | 60  |  |  |  |  |  |  |
| Db                                                                                                                | 1                                                                     | MEYQNESLSPRLKLGKVGKVEIKRIENTTNQVTFCKRRSGLLKKAYELSVLCDAEVAL   | 60  |  |  |  |  |  |  |
| QY                                                                                                                | 61                                                                    | VIFSTRGRLYEYANNSVGRGTIERYKKACSDAVNPPSVTEANTQYQOEASKLRRIQDIQ  | 120 |  |  |  |  |  |  |
| Db                                                                                                                | 61                                                                    | IVFSSRGRLYEYNSDVSKTIERYKKASADSNSTGVSSEANAQYQOEAAKLRQICNLQ    | 120 |  |  |  |  |  |  |
| QY                                                                                                                | 121                                                                   | NSNRHIVGESLGNFKELNLEGRLEKIGISVRSKKNELLVAEIEYMQKREMELOHNNM    | 180 |  |  |  |  |  |  |
| Db                                                                                                                | 121                                                                   | NSNRHMLGEALSSLSVKELSLRLEKIGISIRSKKNELLFAEIEYMQKREVDLHNNQ     | 180 |  |  |  |  |  |  |

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| QY | 181 | YLRAKIAEGARLNPDOQESSVIOGTTVYESGVSSHDSQSHY-NRNYIPVNLLEPNQQFSG | 239 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|----|-----|--------------------------------------------------------------|-----|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|

Job time : 26.1053 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 27, 2003, 12:39:53 ; Search time 9.03644 Seconds  
(without alignments)  
1138.295 Million cell updates/sec

Title: US-09-978-382A-4  
Perfect score: 1263  
Sequence: 1 MEEGSSHDAESSKLGK.....NLLEPNQOQSGDQPPLQLV 248

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID           | Description         |
|------------|-------|-------------|--------|--------------|---------------------|
| 1          | 1263  | 100.0       | 248    | 1 AGL1_ARATH | P29381 arabidopsis  |
| 2          | 1050  | 83.1        | 246    | 1 AGL5_ARATH | P29385 arabidopsis  |
| 3          | 806.5 | 63.9        | 248    | 1 AG_TOBAC   | Q43585 nicotiana t  |
| 4          | 806   | 63.8        | 242    | 1 AG_PANGI   | Q40872 panax ginse  |
| 5          | 798.5 | 63.2        | 248    | 1 AG_LYCES   | Q40168 lycopersico  |
| 6          | 794.5 | 62.9        | 242    | 1 AG_PETHY   | Q40885 petunia hyb  |
| 7          | 752   | 59.5        | 252    | 1 AG_ARATH   | P17839 arabidopsis  |
| 8          | 751   | 59.5        | 252    | 1 AG_BRANA   | Q01540 brassica na  |
| 9          | 678   | 53.7        | 230    | 1 AGL1_ARATH | Q38836 arabidopsis  |
| 10         | 440.5 | 34.9        | 251    | 1 AGL9_ARATH | O22456 arabidopsis  |
| 11         | 433   | 34.3        | 254    | 1 AGL9_SINAL | O04067 sinapis alb  |
| 12         | 430   | 34.0        | 241    | 1 AGL9_PETHY | Q03489 petunia hyb  |
| 13         | 426   | 33.7        | 252    | 1 AGL6_ARATH | P29386 arabidopsis  |
| 14         | 421   | 33.3        | 224    | 1 AGL9_LYCES | Q42464 lycopersico  |
| 15         | 418   | 33.1        | 250    | 1 AGL8_SOLTU | Q42429 solanum tub  |
| 16         | 411.5 | 32.6        | 227    | 1 AGL8_LYCES | Q40170 lycopersico  |
| 17         | 410.5 | 32.5        | 214    | 1 SOCI_ARATH | O64645 arabidopsis  |
| 18         | 408.5 | 32.3        | 233    | 1 CMB1_DIAAC | Q39685 dianthus ca  |
| 19         | 404.5 | 32.0        | 250    | 1 AGL9_ARADE | Q38694 arandha debo |
| 20         | 401   | 31.7        | 258    | 1 AGL3_ARATH | P29383 arabidopsis  |
| 21         | 399.5 | 31.6        | 219    | 1 AGL1_ARATH | O82743 arabidopsis  |
| 22         | 399.5 | 31.6        | 244    | 1 AGL3_ARATH | Q38837 arabidopsis  |
| 23         | 394   | 31.2        | 248    | 1 AGL2_ARATH | P29382 arabidopsis  |
| 24         | 391.5 | 31.0        | 250    | 1 AGL8_SOLCO | O22328 solanum com  |
| 25         | 391   | 31.0        | 254    | 1 API_SINAL  | Q41276 sinapis alb  |
| 26         | 391   | 31.0        | 256    | 1 API_ARATH  | P35631 arabidopsis  |
| 27         | 382.5 | 30.3        | 228    | 1 AGLY_ARATH | Q9szj6 arabidopsis  |
| 28         | 381   | 30.2        | 242    | 1 AGL8_ARATH | Q38876 arabidopsis  |
| 29         | 378.5 | 30.0        | 227    | 1 AGL7_ARATH | Q38840 arabidopsis  |
| 30         | 378   | 29.9        | 250    | 1 AGL4_ARATH | P29384 arabidopsis  |
| 31         | 377   | 29.8        | 241    | 1 AGL8_SINAL | Q41274 sinapis alb  |
| 32         | 376   | 29.8        | 221    | 1 AGL4_ARATH | Q38838 arabidopsis  |
| 33         | 352   | 27.9        | 265    | 1 JOIN_LYCES | Q9fuy6 lycopersico  |

|    |       |      |     |              |                    |
|----|-------|------|-----|--------------|--------------------|
| 34 | 351   | 27.8 | 210 | 1 FBP1_PETHY | Q03488 petunia hyb |
| 35 | 345.5 | 27.4 | 268 | 1 AGL5_ARATH | Q38847 arabidopsis |
| 36 | 343   | 27.2 | 211 | 1 AGL2_ARATH | Q38841 arabidopsis |
| 37 | 341.5 | 27.0 | 264 | 1 AGL5_BRANA | Q39295 brassica na |
| 38 | 340.5 | 27.0 | 209 | 1 GLOB_TOBAC | Q03416 nicotiana t |
| 39 | 339   | 26.8 | 240 | 1 SVP_ARATH  | Q9fvc1 arabidopsis |
| 40 | 332.5 | 26.3 | 215 | 1 GLOB_ANTMA | Q03378 antirrhinum |
| 41 | 318   | 25.2 | 212 | 1 MAD2_PETHY | Q07474 petunia hyb |
| 42 | 309   | 24.5 | 208 | 1 PIST_ARATH | P48007 arabidopsis |
| 43 | 303.5 | 24.0 | 232 | 1 AP3_ARATH  | P35632 arabidopsis |
| 44 | 297.5 | 23.6 | 231 | 1 MAD1_PETHY | Q07472 petunia hyb |
| 45 | 288.5 | 22.8 | 227 | 1 DEFA_ANTMA | P23706 antirrhinum |

ALIGNMENTS

RESULT 1  
AGL1\_ARATH  
ID AGL1\_ARATH STANDARD; PRT; 248 AA.  
AC P29381;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Agamous-like MADS box protein AGL1 (Protein Shatterproof 1).  
GN AGL1 OR SHP1 OR AT3G56780 OR T20N10.130.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91160981; PubMed=1672119;  
RA Ma H., Yanofsky M.F., Meyerowitz E.M.;  
RT "AGL1-AGL6, an Arabidopsis gene family with similarity to floral  
RT homeotic and transcription factor genes.";  
RL Genes Dev. 5:484-495(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RX MEDLINE=21016720; PubMed=11130713;  
RA Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unsel M.,  
RA Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,  
RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,  
RA De Simone V., Choisne N., Artiguenave F., Robert C., Brottier P.,  
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,  
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,  
RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,  
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,  
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,  
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordsiek G.,  
RA Reichelt J., Scharfe M., Schoen O., Barges M., Terol J., Climent J.,  
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,  
RA Cooke R., Laudie M., Berger-Liauro C., Purnelle B., Masuy D.,  
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,  
RA Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,  
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,  
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.-U., Tallon L.J., Jenkins J.,  
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,  
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,  
RA Pai G., Millitscher J., Sellers P., Gill J.E., Feldblyum T.V.,  
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,  
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,  
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,  
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
RA Nakayama S., Nakazaki N., Shippo S., Takeuchi C., Wada T.,  
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;  
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis  
RT thaliana.";  
RL Nature 408:820-822(2000).  
CC -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.  
CC -!- SUBCELLULAR LOCATION: Nuclear.



|                                                              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                   |     |
|--------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------|-----|
| Qy                                                           | 187                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | AEGARLNPDQDES--SVIQGTTVYESGVSHDQSQHYNRNNTIPVNLLPEPNOQFSGQDPP                                      | 244 |
| Db                                                           | 188                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | II I II: :::: II I III: II I : : IIII<br>AETERAQOQQOQMMLPGSSSYELVPPPH---QFDTRNVLQVNGLQTNNHYTRQDPS | 244 |
| Qy                                                           | 245                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | LQLV 248<br>IIII                                                                                  |     |
| Db                                                           | 245                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | LQLV 248                                                                                          |     |
| <br>                                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                   |     |
| RESULT 4                                                     |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                   |     |
| AG_PANGI STANDARD; PRT; 242 AA.                              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                   |     |
| ID                                                           | AG_PANGI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                                                   |     |
| AC                                                           | Q40872;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |                                                                                                   |     |
| DT                                                           | 15-DEC-1998 (Rel. 37, Created)                                                                                                                                                                                                                                                                                                                                                                                                                                                          |                                                                                                   |     |
| DT                                                           | 15-DEC-1998 (Rel. 37, Last sequence update)                                                                                                                                                                                                                                                                                                                                                                                                                                             |                                                                                                   |     |
| DE                                                           | 15-JUN-2002 (Rel. 41, Last annotation update)                                                                                                                                                                                                                                                                                                                                                                                                                                           |                                                                                                   |     |
| DB                                                           | AGAMOUS protein (GAG2).                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |                                                                                                   |     |
| GN                                                           | AG2.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                                                                                                   |     |
| OS                                                           | Panax ginseng (Korean ginseng).                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                   |     |
| OC                                                           | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;                                                                                                                                                                                                                                                                                                                                                                                                                      |                                                                                                   |     |
| OC                                                           | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;                                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                                                   |     |
| OC                                                           | Asteridae; euasterids II; Apiales; Araliaceae; Panax.                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                                   |     |
| OX                                                           | NCBI_TaxId=4054;                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                                                                                                   |     |
| RN                                                           | [1]                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |                                                                                                   |     |
| RP                                                           | SEQUENCE FROM N.A.                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |                                                                                                   |     |
| RC                                                           | TISSUE=Flower;                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |                                                                                                   |     |
| RA                                                           | Kim Y.-S., Lee H.-S., Hoon L.-S., Yoo O.J., Chung W.I., Liu J.R.;                                                                                                                                                                                                                                                                                                                                                                                                                       |                                                                                                   |     |
| RT                                                           | "The cDNA sequence of two MADS box genes in Panax ginseng (GAG2,<br>GAG1).";                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                                                   |     |
| RL                                                           | (In) Plant Gene Register PGR95-060.                                                                                                                                                                                                                                                                                                                                                                                                                                                     |                                                                                                   |     |
| CC                                                           | -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR INVOLVED IN REGULATING GENES THAT DETERMINES STAMEN AND CARPEL DEVELOPMENT IN WILD-TYPE FLOWERS (BY SIMILARITY).                                                                                                                                                                                                                                                                                                                            |                                                                                                   |     |
| CC                                                           | -!- SUBCELLULAR LOCATION: Nuclear (By similarity).                                                                                                                                                                                                                                                                                                                                                                                                                                      |                                                                                                   |     |
| CC                                                           | -!- TISSUE SPECIFICITY: FLOWER. PREFERENTIALLY EXPRESSED IN STAMEN AN CARPEL AND WEAKLY IN PETAL. UNDETECTED IN LEAVES AND ROOTS.                                                                                                                                                                                                                                                                                                                                                       |                                                                                                   |     |
| CC                                                           | -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.                                                                                                                                                                                                                                                                                                                                                                                                             |                                                                                                   |     |
| CC                                                           | -!- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                                   |     |
| CC                                                           | -----                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                                   |     |
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| CC                                                           | -----                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                                   |     |
| DR                                                           | EMBL; Z46612; CAA86585.1; -.                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                                                   |     |
| DR                                                           | HSPB; P11746; LMNM.                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |                                                                                                   |     |
| DR                                                           | TRANSFAC; T03099; -.                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                                                                                                   |     |
| DR                                                           | InterPro; IPR002487; TF_Kbox.                                                                                                                                                                                                                                                                                                                                                                                                                                                           |                                                                                                   |     |
| DR                                                           | InterPro; IPR002100; TF_MADSbox.                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                                                                                                   |     |
| DR                                                           | Pfam; PF00319; SRF-TF; 1.                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                                                                                                   |     |
| DR                                                           | Pfam; PF01486; K-box; 1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                                                   |     |
| DR                                                           | PRINTS; PR00404; MADSDOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                                                   |     |
| DR                                                           | SMART; SM00432; MADS; 1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                                                   |     |
| DR                                                           | PROSITE; PS00350; MADS_BOX_1; 1.                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                                                                                                   |     |
| DR                                                           | PROSITE; PSS0066; MADS_BOX_2; 1.                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                                                                                                   |     |
| KW                                                           | Transcription regulation; DNA-binding; Activator; Nuclear protein.                                                                                                                                                                                                                                                                                                                                                                                                                      |                                                                                                   |     |
| FT                                                           | DOMAIN 19 73 MADS.                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |                                                                                                   |     |
| FT                                                           | DOMAIN 112 184 K-BOX.                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                                   |     |
| SQ                                                           | SEQUENCE 242 AA; 27781 MW; 0B3F02937B24CF76 CRC64;                                                                                                                                                                                                                                                                                                                                                                                                                                      |                                                                                                   |     |
| <br>                                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                   |     |
| Query Match 63.8%; Score 806; DB 1; Length 242;              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                   |     |
| Best Local Similarity 66.7%; Pred. No. 5e-51;                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                   |     |
| Matches 166; Conservative 33; Mismatches 36; Indels 14; Gaps |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                   |     |
| Qy                                                           | 6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | SSHDAES-----SKKLGRGKIETKRIENTNRQVTFCKRRNGLLKAYELSVLCDAEVAL 60                                     |     |
| Db                                                           | 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | IFDYDDQSGNLSPQRKLGRGKIETKRIENTNRQVTFCKRRNGLLKAYELSVLCDAEVAL 61                                    |     |
| Qy                                                           | 61                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | VIFSTRGLRYEYANNSVRGTIERYKKACSDAVNPSPVTANTQYYQOEASKLRRIQDIQ 120                                    |     |







Transcription regulation; DNA-binding; Activator; Nuclear protein.

```
FT DOMAIN 19 73 MADS.
FT DOMAIN 112 184 K-BOX.
FT CONFLICT 1 M -> T (IN REF. 1).
SQ SEQUENCE 252 AA; 28723 MW; 4E7591AD85654C1C CRC64;

Query Match 59.5%; Score 752; DB 1; Length 252;
Best Local Similarity 63.2%; Pred. No. 3.8e-47;
Matches 160; Conservative 33; Mismatches 48; Indels 12; Gaps 5;

QY 2 EEGSSHDAESSKLGKRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVALI 61
DB 6 ELGG---DSSPLRKSGRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVALI 62
QY 62 IFSTRGRLYEYANNSVRGTIERYKACSDAVNPSPVTEANTQYQOEASKLRRQIRDION 121
DB 63 VFSSRGRLYEYSNNVSGTIERYKKAISDNSNTGSAEINAQYQOESAKLRQOIIISIQ 122
QY 122 SNRHIVGESLGNFKELKLNLEGRLEKISRVRSKKNELLVAEIEYMQKREMELOHNNMY 181
DB 123 SNRQLMGETIGSMSPKELNLEGRLEKISRVRSKKNELLVAEIEYMQKREVDLHNDNQI 182
QY 182 LRAKIAEGARLNPDOQESSVIQTTVYESGV-SSHDQSHY-NRNYIPVNLLEPNQOF--- 237
DB 183 LRAKIAENERNNP---SISLMPGGSNYEQLMPPQTPQSPFDSRNYFQVAALQPNHHYS 239
QY 238 --SGQDQPPLQLV 248
DB 240 SAGRQDQTAQLV 252

RESULT 8
AG AG BRANA STANDARD; PRT; 252 AA.
ID AG BRANA
AC Q01540;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE AGAMOUS protein.
GN AG1.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Westar;
RX MEDLINE=93008236; PubMed=1356631;
RA Mandel M.A., Bowman J.L., Kempin S.A., Ma H., Meyerowitz E.M.,
RA Yanofsky M.F.;
RT "Manipulation of flower structure in transgenic tobacco.";
RL Cell 71:133-143(1992).
CC -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR INVOLVED IN REGULATING
CC GENES THAT DETERMINE STAMEN AND CARPEL DEVELOPMENT IN WILD-TYPE
CC FLOWERS.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -!- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
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or send an email to license@isb-sib.ch).
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EMBL; M99415; AAA32985.1; -
DR PIR; A43484; A43484.
DR HSSP; P11746; LMNN.
DR TRANSFAC; T01773; -
DR InterPro; IPR002487; TF_Kbox.
```

```
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF00319; SRF-TF; 1.
DR Pfam; PF01486; K-box; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00666; MADS_BOX_2; 1.
KW Transcription regulation; DNA-binding; Activator; Nuclear protein.
FT DOMAIN 19 73 MADS.
FT DOMAIN 112 184 K-BOX.
SQ SEQUENCE 252 AA; 28778 MW; 7C1EF7C96C19EACE CRC64;

Query Match 59.5%; Score 751; DB 1; Length 252;
Best Local Similarity 62.0%; Pred. No. 4.5e-47;
Matches 158; Conservative 34; Mismatches 49; Indels 14; Gaps 5;

QY 1 MEEGSSHDAESSKLGKRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVAL 60
DB 5 MELGES---SPQKAGRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVAL 61
QY 61 VIFSTRGRLYEYANNSVRGTIERYKACSDAVNPSPVTEANTQYQOEASKLRRQIRDIO 120
DB 62 IVFSSRGRLYEYSNNVSGTIERYKKAISDNSNTGSAEINAQYQOESAKLRQOIIISIQ 121
QY 121 NSNRHIVGESLGNFKELKLNLEGRLEKISRVRSKKNELLVAEIEYMQKREMELOHNNM 180
DB 122 NSNRQLMGETIGSMSPKELNLEGRLEKISRVRSKKNELLVAEIDYMQKREVDLHNDNQ 181
QY 181 YLRKIAEGARLNPDOQESSVIQTTVYESGVSSHDQSHY---NRNYIPVNLLEPNQOF 237
DB 182 LLRAKIAENERNNP---SLMPGGSNYEQ-IMPPTQTPQPFDSRNYFQVAALQPNHHH 237
QY 238 ---SGQDQPPLQLV 248
DB 238 YSSAGREDQTAQLV 252

RESULT 9
AG11 ARATH STANDARD; PRT; 230 AA.
ID AG11 ARATH
AC Q38836;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Agamous-like MADS box protein AGL11.
GN AGL11 OR AT4G09960 OR T5L19.90.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Landsberg erecta; TISSUE=Flower;
RX MEDLINE=96004530; PubMed=7549482;
RA Rounsley S.D., Ditta G.S., Yanofsky M.F.;
RT "Diverse roles for MADS box genes in Arabidopsis development.";
RL Plant Cell 7:1259-1269(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083488; PubMed=10617198;
RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terry N.,
RA Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M.,
RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
RA Kreis M., Delsen M., Puigdomenech P., Watson M., Schmidtheini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hobeisel J., Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
RA Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
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CC -----
DR EMBL: AF015552; AAB67832.1; -.
DR EMBL: AC002396; AAC00586.1; -.
DR HSSP: P11746; 1MNM.
DR TRANSFAC: T03032; -.
DR InterPro: IPR002487; TF_Kbox.
DR InterPro: IPR002100; TF_MADSbox.
DR Pfam: PF00319; SRF-TF; 1.
DR Pfam: PF01486; K-box; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS50066; MADS_BOX_2; 1.
DR Transcription regulation; DNA-binding; Nuclear protein.
KW DOMAIN 3 57 MADS.
FT DOMAIN 100 172 K-BOX.
SQ SEQUENCE 251 AA; 29066 MW; 0057CABD3F1AFC40 CRC64;

Query Match 34.9%; Score 440.5; DB 1; Length 251;
Best Local Similarity 42.4%; Pred. No. 7.1e-25;
Matches 100; Conservative 47; Mismatches 70; Indels 19; Gaps 6;

QY 16 LGRGKIEIKRIENTNRQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGLIYEY-AN 74
   :|||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
Db 1 MGRGRVELKRIENKINRQVTFCKRRNGLLKAYELSVLCDAEVALIIFSNRGLIYFCSS 60

QY 75 NSVRGTIERKKACSDAVNPSPVTE---ANTQYQQEASKLRQIRDIQNSNRHIVGES 130
   :|||:||||| :||| :||| :||| :||| :||| :||| :||| :||| :
Db 61 SSMRLTLYRQK-CNYGAPENVPREALAVELSSQOEYKLRKERYDALQRTQRLNGED 119

QY 131 LGSNFKELKNLEGRLEKGISRVRSKKNELLVAETIYMKREMLQHNMYLRAKIAEG- 189
   ||| :|||:||||| :||| :||| :||| :||| :||| :||| :||| :||| :
Db 120 LGPLSTKELESRLERQDSSLKQIRALRTQFMDQLNDLQSKERMLTETNKTLRRLADGY 179

QY 190 ---ARLNPDOQESSVIQGTYYESGVSSHDSQHYNNRNIYIPVNLEPNQOFSGODQ 242
   :|||:||||| :||| :||| :||| :||| :||| :||| :||| :||| :
Db 180 QMPLQLNPQEE-----VDHYGRHHQQQHSQAFFOPLE-CEPILGIYQOQ 226

RESULT 11
AGL9_SINAL
ID AGL9_SINAL STANDARD; PRT; 254 AA.
AC Q04067;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Agamous-like MADS box protein AGL9 homolog (MADS D).
GN AGL9.
OS Sinapis alba (White mustard) (Brassica hirta).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Sinapis.
OX NCBI_TaxID=3728;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Flower;
RX MEDLINE=97390682; PubMed=9247539;
RA Bonhomme F., Sommer H., Bernier G., Jacquard A.;
RT "Characterization of SaMADS D from Sinapis alba suggests a dual
RT function of the gene: in inflorescence development and floral
RT organogenesis.";
RL Plant Mol. Biol. 34:573-573(1997).
CC -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR ACTIVE IN INFLORESCENCE
CC DEVELOPMENT AND FLORAL ORGANOGENESIS.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -!- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Y08626; CAA69916.1; -.
DR HSSP: P11746; 1MNM.
DR TRANSFAC: T03170; -.
DR InterPro: IPR002487; TF_Kbox.
DR InterPro: IPR002100; TF_MADSbox.
DR Pfam: PF00319; SRF-TF; 1.
DR Pfam: PF01486; K-box; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS50066; MADS_BOX_2; 1.
DR Transcription regulation; DNA-binding; Nuclear protein.
KW DOMAIN 3 57 MADS.
FT DOMAIN 100 172 K-BOX.
SQ SEQUENCE 254 AA; 29603 MW; EDD65155060BFD46 CRC64;

Query Match 34.3%; Score 433; DB 1; Length 254;
Best Local Similarity 40.5%; Pred. No. 2.5e-24;
Matches 100; Conservative 48; Mismatches 71; Indels 28; Gaps 6;

QY 16 LGRGKIEIKRIENTNRQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGLIYEY-AN 74
   :|||:||||| ||||| ||||| ||||| ||||| ||||| ||||| :
Db 1 MGRGRVELKRIENKINRQVTFCKRRNGLLKAYELSVLCDAEVALIIFSNRGLIYFCSS 60

QY 75 NSVRGTIERKKACSDAVNPSPVTE---ANTQYQQEASKLRQIRDIQNSNRHIVGES 130
   :|||:||||| :||| :||| :||| :||| :||| :||| :||| :||| :
Db 61 SSMRLTLYRQK-CNYGPEPVPREALAVELSSQOEYKLRKERYDALQRTQRLNGED 119

QY 131 LGSNFKELKNLEGRLEKGISRVRSKKNELLVAETIYMKREMLQHNMYLRAKIAEG- 189
   ||| :|||:||||| :||| :||| :||| :||| :||| :||| :||| :||| :
Db 120 LGPLSTKELESRLERQDSSLKQIRALRTQFMDQLNDLQSKERMLNETNKTLRRLADGY 179

QY 190 ---ARLNPDOQESSVIQGTYYESGVSSHDSQHYNNRNIYIPVNLE-----PNQOF 237
   :|||:||||| :||| :||| :||| :||| :||| :||| :||| :||| :
Db 180 QMPLQLNPQEDHHVDYG-----RHDQQQQQNSHHAFFQPLECEPILOMGYQGQD 230

QY 238 SGQDQPP 244
   :|||:||||| :||| :||| :||| :||| :||| :||| :||| :||| :
Db 231 HGMEACP 237

RESULT 12
AGL9_PETHY
ID AGL9_PETHY STANDARD; PRT; 241 AA.
AC Q03489;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Agamous-like MADS box protein AGL9 homolog (Floral homeotic protein
DE FBP2) (Floral binding protein 2).
GN FBP2.
OS Petunia hybrida (Petunia).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
OX NCBI_TaxID=4102;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93005737; PubMed=1356537;
RA Angenent G.C., Busscher M., Franken J., Mol J.N.M., van Tunen A.J.;
RT "Differential expression of two MADS box genes in wild-type and
RT mutant petunia flowers.";
RL Plant Cell 4:983-993(1992).
RN [2]
RP REVISIONS TO C-TERMINUS.
RA Angenent G.C.;
RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.
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OS Lycopersicon esculentum (Tomato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=4081;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. VFNT Cherry; TISSUE=Flower;  
RX MEDLINE=93251098; PubMed=1688249;  
RA Pnueli L., Abu-Abeid M., Zamir D., Nacken W., Schwarz-Sommer 2.,  
RA Lifschitz E.;  
RT "The MADS box gene family in tomato: temporal expression during  
RT floral development, conserved secondary structures and homology with  
RT homeotic genes from Antirrhinum and Arabidopsis.";  
RL Plant J. 1:255-266(1991).  
CC -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR ACTIVE IN INFLORESCENCE  
CC DEVELOPMENT AND FLORAL ORGANOGENESIS (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).  
CC -!- TISSUE SPECIFICITY: FLOWER-SPECIFIC.  
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION  
CC FACTORS.  
CC -!- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.  
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CC  
CC EMBL; X60758; CAA43170.1; -.  
DR EMBL; X60480; CAA43010.1; -.  
DR HSSP; P11746; 1MNM.  
DR TRANSFAC; T03187; -.  
DR InterPro; IPR002487; TF\_Kbox.  
DR InterPro; IPR002100; TF\_MADSbox.  
DR Pfam; PF00319; SRF-TF; 1.  
DR Pfam; PF01486; K-box; 1.  
DR PRINTS; PR00404; MADSDOMAIN.  
DR SMART; SM00432; MADS; 1.  
DR PROSITE; PS00350; MADS\_BOX\_1; 1.  
DR PROSITE; PS00350; MADS\_BOX\_2; 1.  
DR PROSITE; PS50066; MADS\_BOX\_2; 1.  
KW Transcription regulation; DNA-binding; Nuclear protein.  
FT DOMAIN 3 57 MADS.  
FT DOMAIN 98 170 K-BOX.  
FT SEQUENCE 224 AA; 25999 MW; 51D10D30867D06F7 CRC64;  
Query Match 33.3%; Score 421; DB 1; Length 224;  
Best Local Similarity 48.1%; Pred. No. 1.5e-23;  
Matches 87; Conservative 43; Mismatches 47; Indels 4; Gaps 3;  
QY 16 LGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGRLYEY-AN 74  
Db 1 MGRGRVQLKRIENKINRQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGRLYEY-AN 74  
QY 75 NSVRGTTIERYKACSDAVNPVSVT--EANTQYQQEASKLRQIRDIQNSNRHI 132  
Db 61 SMKLTLYRYQK-CNYGAPEINISTREALEISSQQEYVKKLGRYEALQRSQRLNLLGEDLG 119  
QY 133 SLNFKELKNLEGRLEKGISVRSKKNELLVAIEYVQKREMLQHNMYLRAKIADGRL 192  
Db 120 PLNSKELESLEQLDMSLKQIRSTRITQLMLDQLTQYQKEHALNEARNTLQRLMEGSQL 179  
QY 193 N 193  
Db 180 N 180  
RESULT 15  
AGL8\_SOLITU STANDARD; PRT; 250 AA.  
ID AGL8\_SOLITU  
AC Q42429;

DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Agamous-like MADS box protein AGL8 homolog (POTM1-1).  
OS Solanum tuberosum (Potato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=4113;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Superior;  
RX MEDLINE=96343939; PubMed=8756601;  
RA Kang S.G., Hannapel D.J.;  
RT "A novel MADS-box gene of potato (Solanum tuberosum L.) expressed  
RT during the early stages of tuberization.";  
RL Plant Mol. Biol. 31:379-386(1996).  
CC -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.  
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).  
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION  
CC FACTORS.  
CC -!- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.  
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CC  
CC EMBL; U23758; AAA92840.1; -.  
DR EMBL; U23757; AAA92839.1; -.  
DR HSSP; P11746; 1MNM.  
DR TRANSFAC; T03145; -.  
DR InterPro; IPR002487; TF\_Kbox.  
DR InterPro; IPR002100; TF\_MADSbox.  
DR Pfam; PF00319; SRF-TF; 1.  
DR Pfam; PF01486; K-box; 1.  
DR PRINTS; PR00404; MADSDOMAIN.  
DR SMART; SM00432; MADS; 1.  
DR PROSITE; PS00350; MADS\_BOX\_1; 1.  
DR PROSITE; PS50066; MADS\_BOX\_2; 1.  
KW Transcription regulation; DNA-binding; Nuclear protein.  
FT DOMAIN 3 57 MADS.  
FT DOMAIN 97 169 K-BOX.  
FT SEQUENCE 250 AA; 28922 MW; EDE37FFFE793DDC4 CRC64;  
Query Match 33.1%; Score 418; DB 1; Length 250;  
Best Local Similarity 39.9%; Pred. No. 2.9e-23;  
Matches 95; Conservative 46; Mismatches 71; Indels 26; Gaps 6;  
QY 16 LGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGRLYEYANN 75  
Db 1 MGRGRVQLKRIENKINRQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGRLYEYANN 75  
QY 76 S-VRGTIERYKK-----ACSDAVNPSPVTEANTQYQQEASKLRQIRDIQNSNRHI 126  
Db 61 SCMERLLERYSYFAERQLVPTDHTSPGWT-----LEHAKLKARLEVLRNQKH 112  
QY 127 VGESLGSNFKELKNLEGRLEKGISVRSKKNELLVAIEYVQKREMLQHNMYLRAKI 186  
Db 113 VGEDLSNFKELKNLEGRLEKGISVRSKKNELLVAIEYVQKREMLQHNMYLRAKI 172  
QY 187 AEG----ARLNP-DQESSVIQGTIVYSGVSSHQSOHYNRYIPVNLLEPNQOFSG 239  
Db 173 KEREKEVAQQNQWDQONHEINSSTFVLPPQL---DSPHLGEAYQNTNVVDNGEVEGG 226  
Search completed: January 27, 2003, 12:44:40  
Job time : 10.0364 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 27, 2003, 12:39:53 ; Search time 8.96356 Seconds  
(without alignments)  
1138.295 Million cell updates/sec

Title: US-09-978-382a-6  
Perfect score: 1242  
Sequence: 1 MEGGASNEVAESSKIGRGK.....NLLEPNQSSNQDPPPLQLV 246

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID           | Description        |
|------------|-------|-------------|--------|--------------|--------------------|
| 1          | 1242  | 100.0       | 246    | 1 AGL5_ARATH | P29385 arabidopsis |
| 2          | 1050  | 84.5        | 248    | 1 AGL1_ARATH | P29381 arabidopsis |
| 3          | 780.5 | 62.8        | 248    | 1 AG_TOBAC   | Q43585 nicotiana t |
| 4          | 772.5 | 62.2        | 242    | 1 AG_PANGI   | Q40872 panax ginse |
| 5          | 770.5 | 62.0        | 248    | 1 AG_LYCES   | Q40168 lycopersico |
| 6          | 767.5 | 61.8        | 242    | 1 AG_PETHY   | Q40885 petunia hyb |
| 7          | 714.5 | 57.5        | 252    | 1 AG_ARATH   | P17839 arabidopsis |
| 8          | 710.5 | 57.2        | 252    | 1 AG_BRANA   | Q01540 brassica na |
| 9          | 704.5 | 56.7        | 230    | 1 AGL1_ARATH | Q38836 arabidopsis |
| 10         | 427   | 34.4        | 252    | 1 AGL6_ARATH | P29386 arabidopsis |
| 11         | 411   | 33.1        | 214    | 1 SOC1_ARATH | O64645 arabidopsis |
| 12         | 407.5 | 32.8        | 241    | 1 AGL9_PETHY | Q03489 petunia hyb |
| 13         | 405   | 32.6        | 250    | 1 AGL8_SOLTU | Q42429 solanum tub |
| 14         | 402.5 | 32.4        | 248    | 1 AGL2_ARATH | P29382 arabidopsis |
| 15         | 401   | 32.3        | 224    | 1 AGL9_LYCES | Q42464 lycopersico |
| 16         | 401   | 32.3        | 233    | 1 CMB1_DIACA | Q39685 dianthus ca |
| 17         | 399.5 | 32.2        | 219    | 1 AGL9_ARATH | O82743 arabidopsis |
| 18         | 397.5 | 32.0        | 250    | 1 AGL9_ARADE | Q38694 aranda debo |
| 19         | 396.5 | 31.9        | 227    | 1 AGL8_LYCES | Q40170 lycopersico |
| 20         | 394.5 | 31.8        | 251    | 1 AGL9_ARATH | O22456 arabidopsis |
| 21         | 393.5 | 31.7        | 244    | 1 AGL3_ARATH | Q38837 arabidopsis |
| 22         | 389   | 31.3        | 250    | 1 AGL4_ARATH | P29384 arabidopsis |
| 23         | 386   | 31.1        | 254    | 1 AGL9_SINAL | O40067 sinapis alb |
| 24         | 385.5 | 31.0        | 258    | 1 AGL3_ARATH | P29383 arabidopsis |
| 25         | 383.5 | 30.9        | 250    | 1 AGL8_SOLCO | O22328 solanum com |
| 26         | 382   | 30.8        | 256    | 1 APL1_ARATH | P35631 arabidopsis |
| 27         | 378   | 30.4        | 242    | 1 AGL8_ARATH | Q38876 arabidopsis |
| 28         | 377   | 30.4        | 241    | 1 AGL8_SINAL | Q41274 sinapis alb |
| 29         | 376.5 | 30.3        | 254    | 1 APL1_SINAL | Q41276 sinapis alb |
| 30         | 376   | 30.3        | 221    | 1 AGL4_ARATH | Q38838 arabidopsis |
| 31         | 372.5 | 30.0        | 228    | 1 AGL1_ARATH | Q9szj6 arabidopsis |
| 32         | 371   | 29.9        | 227    | 1 AGL7_ARATH | Q38840 arabidopsis |
| 33         | 345   | 27.8        | 211    | 1 AGL2_ARATH | Q38841 arabidopsis |

## RESULT 1

## AGL5\_ARATH

ID AGL5\_ARATH STANDARD; PRT; 246 AA.

AC P29385; Q9SJH3;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Agamous-like MADS box protein AGL5.

GN AGL5 OR AT2G24830 OR F7D19.17.

OS Arabidopsis thaliana (Mouse-ear cross).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI\_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91160981; PubMed=1672119;

RA Ma H., Yanofsky M.F., Meyerowitz E.M.;

RT "AGL1-AGL6, an Arabidopsis gene family with similarity to floral

homeotic and transcription factor genes.";

RL Genes Dev. 5:484-495(1991).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=cv Columbia;

RX MEDLINE=20083487; PubMed=10617197;

RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,

RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,

RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,

RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,

RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,

RA Venter J.C.;

RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis

thaliana.";

RL Nature 402:761-768(1999).

CC -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.

CC -!- SUBCELLULAR LOCATION: Nuclear.

CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION

FACTORS.

CC -!- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.

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CC EMBL; M55553; AAA32735.1; -.

CC EMBL; AC006931; AAD21741.2; -.

CC PIR; E39534; E39534.

CC HSSP; P11746; 1MNM.

CC TRANSFAC; T03028; -.

CC InterPro; IPR002487; TF\_Kbox.

## ALIGNMENTS

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DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF00319; SRF-TF; 1.
DR Pfam; PF01486; K-box; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
KW Transcription regulation; DNA-binding; Nuclear protein.
FT DOMAIN 18 72 MADS.
FT DOMAIN 111 183 K-BOX.
SQ SEQUENCE 246 AA; 28157 MW; D4D59316D55606D9 CRC64;

Query Match 100.0%; Score 1242; DB 1; Length 246;
Best Local Similarity 100.0%; Pred. No. 1.3e-79;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MEGGASNEVAESSKKIGRGKIEIKRIENTTNRQVTFCKRRNGLLKAYELSVLCDAEVAL 60

QY 61 VIFSTRGRLEYANNVSRGTTIERYKKACSDAVNPPTITEANTQYYQOEASKLRQIRDIQ 120
DB 61 VIFSTRGRLEYANNVSRGTTIERYKKACSDAVNPPTITEANTQYYQOEASKLRQIRDIQ 120

QY 121 NLNRHILGESLGSNFKELKNLESRLKGISRVRSKKHEMLVAETIYMQKREIELQNDNM 180
DB 121 NLNRHILGESLGSNFKELKNLESRLKGISRVRSKKHEMLVAETIYMQKREIELQNDNM 180

QY 181 YLRSKTERTGLQQESSVTHOGTVYSGVTSSSHQSGQYNNYIAVNLLEPNQNSNQDQ 240
DB 181 YLRSKTERTGLQQESSVTHOGTVYSGVTSSSHQSGQYNNYIAVNLLEPNQNSNQDQ 240

QY 241 PPLQLV 246
DB 241 PPLQLV 246

RESULT 2
AGL1_ARATH STANDARD; PRT; 248 AA.
ID AGL1_ARATH
AC P29381;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Agamous-like MADS box protein AGL1 (Protein Shatterproof 1).
GN AGL1 OR SHP1 OR AT3G58780 OR T20N10.130.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91160981; PubMed=1672119;
RT Ma H., Yanofsky M.F., Meyerowitz E.M.;
RT "AGL1-AGL6, an Arabidopsis gene family with similarity to floral
RT homeotic and transcription factor genes.";
RL Genes Dev. 5:484-495(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unseld M.,
RA Farman B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
RA Delseny M., Boutry M., Griwell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Choisine N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
RA Conrad A., Hornischer K., Kauer G., Loehert T.-H., Nordsiek G.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
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RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Laudie M., Berger-Ilauro C., Purnelle B., Masuy D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Argirion A., Flores M., Liguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rüd S., Zaccaria P., Jenkins J.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Shea T.P.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Van Aken S.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:820-822(2000).
CC -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -!- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
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CC -----
DR EMBL; M55550; AAA32730.1; -.
DR EMBL; AL353032; CAB88295.1; -.
DR PIR; A39534; A39534.
DR HSSP; P11746; IMNM.
DR TRANSFAC; T03022; -.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF00319; SRF-TF; 1.
DR Pfam; PF01486; K-box; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
KW Transcription regulation; DNA-binding; Nuclear protein.
FT DOMAIN 18 72 MADS.
FT DOMAIN 111 183 K-BOX.
SQ SEQUENCE 248 AA; 28336 MW; D377C47F231F2099 CRC64;

Query Match 84.5%; Score 1050; DB 1; Length 248;
Best Local Similarity 85.5%; Pred. No. 2.7e-66;
Matches 212; Conservative 12; Mismatches 22; Indels 2; Gaps 1;

QY 1 MEGGASNEVAESSKKIGRGKIEIKRIENTTNRQVTFCKRRNGLLKAYELSVLCDAEVAL 60
DB 1 MEGGSSHDAESSKKLGRGKIEIKRIENTTNRQVTFCKRRNGLLKAYELSVLCDAEVAL 60

QY 61 VIFSTRGRLEYANNVSRGTTIERYKKACSDAVNPPTITEANTQYYQOEASKLRQIRDIQ 120
DB 61 VIFSTRGRLEYANNVSRGTTIERYKKACSDAVNPPTITEANTQYYQOEASKLRQIRDIQ 120

QY 121 NLNRHILGESLGSNFKELKNLESRLKGISRVRSKKHEMLVAETIYMQKREIELQNDNM 180
DB 121 NSNRHIVGESLGSNFKELKNLEGRLEKGISRVRSKKNELVAETIYMQKREIMELQNNM 180

QY 181 YLRSKITE--RTGLQQESSVTHOGTVYSGVTSSSHQSGQYNNYIAVNLLEPNQNSNQ 238
DB 181 YLRAKIAEGARLNPDQOESSVIQTTVYSGVSSHQSQHYNNRNPVNLLEPNQOFSQ 240

QY 239 DQPPLQLV 246
DB 241 DQPPLQLV 248
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RESULT 3
AG_TOBAC
ID AG_TOBAC STANDARD; PRT; 248 AA.
AC Q43585;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE AGAMOUS protein (NAG1).
GN AG1.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Samsun; TISSUE=stamen;
RX MEDLINE=94120000; PubMed=7507255;
RA Kempin S.A., Mandel M.A., Yanofsky M.F.;
RT "Conversion of the perianth into reproductive organs by ectopic
RL Plant Physiol. 103:1041-1046(1993).
CC -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR INVOLVED IN REGULATING
CC GENES THAT DETERMINES STAMEN AND CARPEL DEVELOPMENT IN WILD-TYPE
CC FLOWERS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -!- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
CC -----
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CC -----
DR EMBL; L23925; AAA17033.1; -
DR HSSP; P11746; 1MNM.
DR TRANSFAC; T03106; -.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF00319; SRF-TF; 1.
DR Pfam; PF01486; K-box; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
DR Transcription regulation; DNA-binding; Activator; Nuclear protein.
FT DOMAIN 19 73 MADS.
FT DOMAIN 112 184 K-BOX.
FT DOMAIN 194 201 POLY-GLN.
SQ SEQUENCE 248 AA; 28664 MW; 10BD24A4CB941402 CRC64;

Query Match 62.8%; Score 780.5; DB 1; Length 248;
Best Local Similarity 66.9%; Pred. No. 1.3e-47;
Matches 158; Conservative 34; Mismatches 39; Indels 5; Gaps 3;

QY 14 KKIGRGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLYEYA 73
DB 15 RKLGRGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLYEYA 74
QY 74 NNSVGTIERYKKACSDAVNPPTITEANTQYQOEASKLRQIRDIQNLRHILGESLGS 133
DB 75 NNSVKATIERYKKACSDSSNTSGISEANAQYQOEASKLRQIRDIQNLRHILGESLGS 134
QY 134 LNFKELKNLESLEKGISRSVRSKKHEMLVAEYEMQKREIEIQNDNNMYLRSKI--TERTG 191
DB 135 LSLRLKLNLEQKIEKGISRSKKNELLFAETIEMQKREIDLNHNNQYLRAKIAETERAQ 194

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QY 192 LQQQESSV-IHQGTVYESGVTSSHQSGQYNNRYIAVNLLPEPNQSSNQDPPLOLV 246
DB 195 QQQQQQQMNLMPGSSSYELVPPPHQFD--TRNYLQVNGLQTNHNYTRQDQPSLQLV 248

RESULT 4
AG_PANGI
ID AG_PANGI STANDARD; PRT; 242 AA.
AC Q40872;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE AGAMOUS protein (GAG2).
GN AG2.
OS Panax ginseng (Korean ginseng).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Apiales; Araliaceae; Panax.
OX NCBI_TaxID=4054;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Flower;
RA Kim Y.S., Lee H.S., Hoon L.S., Yoo O.J., Chung W.I., Liu J.R.;
RT "The cDNA sequence of two MADS box genes in Panax ginseng (GAG2,
RL (in) Plant Gene Register PGR95-060.
CC -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR INVOLVED IN REGULATING
CC GENES THAT DETERMINES STAMEN AND CARPEL DEVELOPMENT IN WILD-TYPE
CC FLOWERS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- TISSUE SPECIFICITY: FLOWER. PREFERENTIALLY EXPRESSED IN STAMEN AND
CC CARPEL AND WEAKLY IN PETAL. UNDETECTED IN LEAVES AND ROOTS.
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -!- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
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CC -----
DR EMBL; Z46612; CAA86585.1; -
DR HSSP; P11746; 1MNM.
DR TRANSFAC; T03099; -.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF00319; SRF-TF; 1.
DR Pfam; PF01486; K-box; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
DR Transcription regulation; DNA-binding; Activator; Nuclear protein.
FT DOMAIN 19 73 MADS.
FT DOMAIN 112 184 K-BOX.
SQ SEQUENCE 242 AA; 27781 MW; 0B3F02937B24CF76 CRC64;

Query Match 62.2%; Score 772.5; DB 1; Length 242;
Best Local Similarity 66.1%; Pred. No. 4.7e-47;
Matches 154; Conservative 34; Mismatches 40; Indels 5; Gaps 2;

QY 14 KKIGRGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLYEYA 73
DB 15 RKLGRGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLYEYA 74
QY 74 NNSVGTIERYKKACSDAVNPPTITEANTQYQOEASKLRQIRDIQNLRHILGESLGS 133
DB 75 NNSVGTIERYKKACSDSPNTSSVSEANAQYQOEASKLRQIRDIQNLRHILGESLGS 134
QY 134 LNFKELKNLESLEKGISRSVRSKKHEMLVAEYEMQKREIEIQNDNNMYLRSKITERGLQ 193

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QY 123 NRHILGESLGNFKELNLESLRLEKISRVRSKKHEMLVAEIEYMKREIELOQNDNMYL 182
Db 124 NRQLMGETIGSMSPKELRNLEGRLESLRSIRSKKNELLFSEIDYMQKREVDLHNDNQIL 183
QY 183 RSKITERTGLQQQESSVHHQGTVVESGVTSSHQSGQ--YNNRYTAVNLLLEPN-----QNSS 236
Db 184 RAKIAENE-RNNPSISLMPGGSNYEQLMPPPTQSPQFDSRNYFQVAALQPNHHYSAG 242
QY 237 NQDQPPQLQV 246
Db 243 RDQQTALQLV 252
RESULT 8
AG_BRNA
ID AG_BRNA STANDARD; PRT; 252 AA.
AC Q01540;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE AGAMOUS protein.
GN AG1.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Westar;
RX MEDLINE=93008236; PubMed=1356631;
RA Mandel M.A., Bowman J.L., Kempin S.A., Ma H., Meyerowitz E.M.,
RA Yanofsky M.F.;
RT "Manipulation of flower structure in transgenic tobacco.";
RL Cell 71:133-143(1992).
CC -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR INVOLVED IN REGULATING
CC GENES THAT DETERMINES STAMEN AND CARPEL DEVELOPMENT IN WILD-TYPE
CC FLOWERS.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -!- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
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EMBL; M99415; AAA32985.1; -.
PIR; A43484; A43484.
HSP; P11746; 1MNM.
TRANSFAC; T01773; -.
InterPro; IPR002487; TF_Kbox.
InterPro; IPR002100; TF_MADSbox.
Pfam; PF00319; SRF-TF; 1.
Pfam; PF01486; K-box; 1.
PRINTS; PR00404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
Transcription regulation; DNA-binding; Activator; Nuclear protein.
DOMAIN 19 73 MADS.
DOMAIN 112 184 K-BOX.
SEQUENCE 252 AA; 28778 MW; 7C1EF7C96C19EACE CRC64;
Query Match 57.2%; Score 710.5; DB 1; Length 252;
Best Local Similarity 58.4%; Pred. No. 9.8e-43;
Matches 146; Conservative 39; Mismatches 54; Indels 11; Gaps 4;
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QY 3 GGASNEVAESSKKIGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVALVI 62
Db 8 GGESS----PQKAGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVALIV 63
QY 63 FSTRGRLYEVANNVSRGTYERYKKACSDAVNPPTITEANTQYQQEASKLRQIRDQNL 122
Db 64 FSSGRLYEYSNNSVKGTYERYKKAISDNSNTGSAEINAQYQQESAKLRQIISQNS 123
QY 123 NRHILGESLGNFKELNLESLRLEKISRVRSKKHEMLVAEIEYMKREIELOQNDNMYL 182
Db 124 NRQLMGETIGSMSPKELRNLEGRLESLRSIRSKKNELLFSEIDYMQKREVDLHNDNQIL 183
QY 183 RSKITERTGLQQQESSVHHQGTVVESGVTSSHQSGQ--YNNRYTAVNLLLEPN-----QNSS 236
Db 184 RAKIAENE-RNNPSISLMPGGSNYEQIMPPPTQSPQFDSRNYFQVAALQPNHHYSAG 242
QY 237 NQDQPPQLQV 246
Db 243 RDQQTALQLV 252
RESULT 9
AG11_ARATH
ID AG11_ARATH STANDARD; PRT; 230 AA.
AC Q38836;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Agamous-like MADS box protein AGL11.
GN AGL11 OR AT4G09960 OR T5L19.90.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Landsberg erecta; TISSUE=Flower;
RX MEDLINE=96004530; PubMed=7549482;
RA Rounsley S.D., Ditta G.S., Yanofsky M.F.;
RT "Diverse roles for MADS box genes in Arabidopsis development.";
RL Plant Cell 7:1259-1269(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083488; PubMed=10617198;
Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M.,
Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
Kreis M., Delsen M., Puigdomenech P., Watson M., Schmidtheini T.,
Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
Langham S.-A., McCullagh B., Bilham L., Robben J.,
Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
Weitzenegger T., Bothe G., Ransperger U., Hilbert H., Braun M.,
Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
Van Montagu M., Rogers J., Cronin J., Quail M., Bray-Allen S.,
Clark L., Doggett J., Hall S., Kay M., Lennard N., McClay K., Mayes R.,
Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
Borkova D., Bloeker H., Scharfe M., Grimm M., Loehner T.-H.,
Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
Gabel C., Fuchs M., Fartmann B., Ganderath K., Dauner D., Herzl A.,
Massenet O., Quigley F., Clabaud G., Muendlein A., Feilber R.,
Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
Chedfor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,
Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
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RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Biele C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Stokem M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dente M., Pepin K., Hillier L.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
RA Antoniou B., Zidan M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Chen E., Marra M., Martienssen R., McCombie W.R.,
RA "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:769-777(1999).
CC -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -!- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
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CC -----
DR EMBL; U20182; AAC49080.1; -.
DR EMBL; AL049481; CAB39620.1; -.
DR EMBL; AL161516; CAB78119.1; -.
DR HSSP; P11746; 1MNM.
DR TRANSFAC; T03009; -.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF00319; SRF-TF; 1.
DR Pfam; PF01486; K-box; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
KW Transcription regulation; DNA-binding; Nuclear protein.
FT DOMAIN 3 57 MADS.
FT DOMAIN 96 168 K-BOX.
SQ SEQUENCE 230 AA; 26183 MW; 336C383355E6CB51 CRC64;

Query Match 56.7%; Score 704.5; DB 1; Length 230;
Best Local Similarity 62.2%; Pred. No. 2.3e-42;
Matches 138; Conservative 33; Mismatches 44; Indels 7; Gaps 1;

QY 16 IGRGKIEIKRIENTTNRQVTFCKRRNGLLKAYELSVLCDAEVALVFSTRGRLYEYANN 75
Db 1 MGRGKIEIKRIENTTNRQVTFCKRRNGLLKAYELSVLCDAEVALVFSTRGRLYEYANN 60

QY 76 SVRGTIERYKKACSDAVNPPTITEANTQYQOEASKLRQRTDIQNLRHILGESLSLN 135
Db 61 NIRSTIERYKKACSDSTNTSTVQYQOESAKLRQQTQITQNTSNRNLMDGSLSSLS 120

QY 136 FKLKNLESLEKGISRVRSKKHEMLVAEYEMQKREIEIFQNDNMYLRSKITERGLQQQ 195
Db 121 VKELQVENLEKATSRIRSKKHELLVEITENAKREIENLNIYLRKVAEVEYQQH 180

QY 196 ESSVIHQGVYSGVTSSSHQSGQYNNRYTAVNLLPQNQSSN 237
Db 181 HQQV-----SCSEINAEALASRNYFAHSIMTAGSGSN 215

RESULT 10

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AGL6_ARATH
ID AGL6_ARATH STANDARD; PRT; 252 AA.
AC P29386;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Agamous-like MADS box protein AGL6.
GN AGL6 OR AT2G45650 OR F17K2.18.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91160981; PubMed=1672119;
RA Ma H., Yanofsky M.F., Meyerowitz E.M.;
RT "AGL1-AGL6, an Arabidopsis gene family with similarity to floral
RT homeotic and transcription factor genes.";
RL Genes Dev. 5:484-495(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768(1999).
CC -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -!- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
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CC -----
DR EMBL; M55554; AAA79328.1; -.
DR EMBL; AC003680; AAC06173.1; -.
DR PIR; F39534; F39534.
DR HSSP; P11831; 1SR5.
DR TRANSFAC; T03029; -.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF00319; SRF-TF; 1.
DR Pfam; PF01486; K-box; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
KW Transcription regulation; DNA-binding; Nuclear protein.
FT DOMAIN 3 57 MADS.
FT DOMAIN 95 167 K-BOX.
SQ SEQUENCE 252 AA; 28744 MW; F763A4A71515CF20 CRC64;

Query Match 34.4%; Score 427; DB 1; Length 252;
Best Local Similarity 42.7%; Pred. No. 4.5e-23;
Matches 100; Conservative 42; Mismatches 74; Indels 18; Gaps 6;

QY 16 IGRGKIEIKRIENTTNRQVTFCKRRNGLLKAYELSVLCDAEVALVFSTRGRLYEYANN 75
:||||:||||| ||||| ||||||||| ||||||||| ||||||| :

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Db 1 MGRGRVEMKRIENKINQVTFKRRNGLLKKAYELSVLCLDAEVALIIFSSRGKLYEFGSV 60

Qy 76 SVRGTIERYKKA--CSDAVNPPTTEANTQYQOEASKLRRQIRDIQNLNRHILGESLGS 133

Db 61 GIESIERNRCYNSLSNNKP---EETQSWCQEVTKLSKYSVLRTNRNLGDLGE 117

Qy 134 LNFELKNLESRLKRGISVRSKKHEMLVAEIEYMQKREIELQNDNMNMYLSKRTERTGLQ 193

Db 118 MGVELQALERQLEAALTATRQRTQVMMEMEDLRKKERQLGDINKQKIKF-ETEG-- 174

Qy 194 QOESSVIHQGVYESSGVTSSHQ--GQVNRNYIAVNLLPNQNSNQDQPPQLQ 245

Db 175 -----HAFKTFQDLWANSAAVAGDPNNSFPVPSHPNVLDCN-TEPFLQI 220

RESULT 11

SOCI\_ARATH

ID SOCI\_ARATH STANDARD; PRT; 214 AA.

AC O64645;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE SUPPRESSOR OF CONSTANS OVEREXPRESSION 1 protein (Agamous-like MADS box protein AGL20).

GN SOCI OR AGL20 OR AT2G45660 OR F17K2.19.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC euroids II; Brassicales; Brassicaceae; Arabidopsals.

OX NCBI\_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20571356; PubMed=11123798;

RA Borner R., Kampmann G., Chandler J., Gleissner R., Wisman E., Apel K., Melzer S.;

RA "A MADS domain gene involved in the transition to flowering in Arabidopsis.";

RT Plant J. 24:591-599(2000).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia;

RX MEDLINE=20083487; PubMed=10617197;

RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M., Venter J.C.;

RA "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.";

RT Nature 402:761-768(1999).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia;

RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;

RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the SSP consortium (Salk/Stanford/PCEC).";

RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

RN [4]

RP FUNCTION.

RC STRAIN=cv. Landsberg erecta;

RX MEDLINE=20450897; PubMed=10995392;

RA Lee H., Suh S.S., Park E., Cho E., Ahn J.H., Kim S.G., Lee J.S., Kwon Y.M., Lee I.;

RA "The AGAMOUS-LIKE 20 MADS domain protein integrates floral inductive pathways in Arabidopsis.";

RT Genes Dev. 14:2366-2376(2000).

RL -1- FUNCTION: Probable transcription factor active in flowering time control. May integrate signals from the photoperiod, vernalization and autonomous floral induction pathways.

CC and autonomous floral induction pathways.

CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).

CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED. NOT FOUND IN THE APICAL MERISTEM OF SHORT-DAY GROWN PLANTS IN VEGETATIVE STAGE.

CC -1- DEVELOPMENTAL STAGE: RAPIDLY UP-REGULATED IN APICAL MERISTEMS DURING THE TRANSITION TO FLOWERING.

CC -1- INDUCTION: UPREGULATED BY GIBBERELLINS, VERNALIZATION AND UNDER LONG-DAY CONDITIONS. GRADUAL INCREASE DURING VEGETATIVE GROWTH.

CC -1- MISCELLANEOUS: LOSS-OF-FUNCTION MUTANTS (T-DNA INSERTION) ARE LATE-FLOWERING.

CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.

CC -1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.

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CC -----

DR EMBL; AC003680; AAC06175.1; -

DR EMBL; AY007726; AAG16297.1; -

DR EMBL; AF385731; AAK60321.1; -

DR HSSP; P11746; 1MNM.

DR TRANSFAC; T04727; -

DR InterPro; IPR002487; TF\_Kbox.

DR InterPro; IPR002100; TF\_MADSbox.

DR Pfam; PF00319; SRF-TF; 1.

DR Pfam; PF01486; K-box; 1.

DR PRINTS; PR00404; MADSDOMAIN.

DR SMART; SM00432; MADS; 1.

DR PROSITE; PS00350; MADS\_BOX\_1; 1.

DR PROSITE; PS00666; MADS\_BOX\_2; 1.

KW Transcription regulation; DNA-binding; Flowering;

KW Developmental protein; Nuclear protein.

FT DOMAIN 3 57 MADS.

FT DOMAIN 72 173 K-BOX.

SQ SEQUENCE 214 AA; 24533 MW; B4D39151DE541F8D CRC64;

Query Match 33.1%; Score 411; DB 1; Length 214;

Best Local Similarity 43.0%; Pred. No. 4.8e-22;

Matches 77; Conservative 51; Mismatches 47; Indels 4; Gaps 1;

Qy 18 RGKIELKRIENTTNQVTFCKRRNGLLKKAYELSVLCLDAEVALIIFSTRGRLYEYANNSV 77

Db 3 RGKTQMKRIENATSRQVTFCKRRNGLLKKAYELSVLCLDAEVALIIFSPKGLYEFASNNM 62

Qy 78 RGTIERKKACSDAVNPPTTEANTQYQOEASKLRRQIRDIQNLNRHILGESLGSNFK 137

Db 63 QDTIDYLRHTKDRYSTKPVSENNQHLKYEAAANMMKKIEQLEASKRKLLEGIGTCSIE 122

Qy 138 ELKNLESRLKRGISVRSKKHEMLVAEIEYMQKREIELQNDNMNMYLSKRTERTGLQOE 196

Db 123 ELQIEQOLEKSVKICIRARKTQVFKQIEQLKQEKALAAEN---EKLSEKWSGHESE 177

RESULT 12

AGL9\_PETHY

ID AGL9\_PETHY STANDARD; PRT; 241 AA.

AC Q03489;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Agamous-like MADS box protein AGL9 homolog (Floral homeotic protein FBP2) (Floral binding protein 2).

GN FBP2.

OS Petunia hybrida (Petunia).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.

OX NCBI\_TaxID=4102;

RN [1]



RP SEQUENCE FROM N.A.  
RX MEDLINE=93005737; PubMed=1356537;  
RA Angenent G.C., Busscher M., Franken J., Mol J.N.M., van Tunen A.J.;  
RT "Differential expression of two MADS box genes in wild-type and  
mutant petunia flowers.";   
RL Plant Cell 4:983-993(1992).  
RN [2]  
RP REVISIONS TO C-TERMINUS.  
RA Angenent G.C.;  
RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION  
CC FACTORS.  
CC -!- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
DR EMBL; M91666; AAA86854.1; -;  
DR PIR; JQ1690; JQ1690.  
DR HSSP; P11746; IMNW.  
DR TRANSFAC; T03093; -;  
DR InterPro; IPR002487; TF\_Kbox.  
DR InterPro; IPR002100; TF\_MADSbox.  
DR Pfam; PF00319; SRF-TF; 1.  
DR Pfam; PF01486; K-box; 1.  
DR PRINTS; PR00404; MADSDOMAIN.  
DR SMART; SM00432; MADS; 1.  
DR PROSITE; PS00350; MADS\_BOX\_1; 1.  
DR PROSITE; PS50066; MADS\_BOX\_2; 1.  
DR PROSITE; PS50066; MADS\_BOX\_2; 1.  
KW Transcription regulation; DNA-binding; Nuclear protein.  
FT DOMAIN 3 57 MADS.  
FT DOMAIN 98 170 K-BOX.  
SQ SEQUENCE 241 AA; 27562 MW; B575BE9468D310BB CRC64;

Query Match 32.8%; Score 407.5; DB 1; Length 241;  
Best Local Similarity 43.3%; Pred. No. 9.6e-22;  
Matches 91; Conservative 48; Mismatches 62; Indels 9; Gaps 5;  
  
QY 16 IGRGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLYEY-AN 74  
Db :|||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :|||: |||:  
1 MGRGRVQLKRIENKINQVTFKRRNGLLKAYELSVLCDAEVALVIFSTRGRLYEY-AN 60  
  
QY 75 NSVRGTIERKKACSDAVNPPTIT--EANTQYQQEASKLRQIRDIQNLNRHILGESLG 132  
Db :|||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :|||: |||:  
61 SSMKLTIERYQK-CNYGAPETNISTREALEISQQEYVLLKARYEALQSRNLLGEDLG 119  
  
QY 133 SLNFKELKNLESRLKGISRVRSKKHEMLVAEIEYMQKRETELQNDNMYLRSKITERT-- 190  
Db :|||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :|||: |||:  
120 PLNSKELESRLQDMSLKQIRSTRQTLMDQLDLQKKEHALNEANRTLKORLMEGSTL 179  
  
QY 191 GLOQQESSVHQGTYESGVTSSSHQSGQYNN 220  
Db :|||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :|||: |||:  
180 NLQWQQA---QDVGYGRQATQTQGDGFH 206

RESULT 13  
AGL8\_SOLTU  
ID AGL8\_SOLTU STANDARD; PRT; 250 AA.  
AC Q42429;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Agamous-like MADS box protein AGL8 homolog (POTM1-1).  
OS Solanum tuberosum (Potato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=4113;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Superior;  
RX MEDLINE=96343939; PubMed=87566601;  
RA Kang S.G., Hannapel D.J.;  
RT "A novel MADS-box gene of potato (Solanum tuberosum L.) expressed  
during the early stages of tuberization.";   
RL Plant Mol. Biol. 31:379-386(1996).  
CC -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.  
CC -!- SUBCELLULAR LOCATION: Nuclear (by similarity).  
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION  
CC FACTORS.  
CC -!- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.  
CC  
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CC  
DR EMBL; U23758; AAA92840.1; -;  
DR EMBL; U23757; AAA92839.1; -;  
DR HSSP; P11746; IMNW.  
DR TRANSFAC; T03145; -;  
DR InterPro; IPR002487; TF\_Kbox.  
DR InterPro; IPR002100; TF\_MADSbox.  
DR Pfam; PF00319; SRF-TF; 1.  
DR Pfam; PF01486; K-box; 1.  
DR PRINTS; PR00404; MADSDOMAIN.  
DR SMART; SM00432; MADS; 1.  
DR PROSITE; PS00350; MADS\_BOX\_1; 1.  
DR PROSITE; PS50066; MADS\_BOX\_2; 1.  
KW Transcription regulation; DNA-binding; Nuclear protein.  
FT DOMAIN 3 57 MADS.  
FT DOMAIN 97 169 K-BOX.  
SQ SEQUENCE 250 AA; 28922 MW; EDE37FFFE793DDC4 CRC64;  
  
Query Match 32.6%; Score 405; DB 1; Length 250;  
Best Local Similarity 39.3%; Pred. No. 1.5e-21;  
Matches 94; Conservative 47; Mismatches 74; Indels 24; Gaps 6;  
  
QY 16 IGRGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLYEYANN 75  
Db :|||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :|||: |||:  
1 MGRGRVQLKRIENKINQVTFKRRSGLLKKAHEISVLCDAEVALVIFSTRGRLYEYANN 60  
  
QY 76 S-VRGTIERYKK-----ACSDAVNPPTITEANTQYQQEASKLRQIRDIQNLNRHI 126  
Db :|||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :|||: |||:  
61 SCMERLLERYERYSFAERQVLVPTDHTSPGWSWT-----LEHAKLKARLEVLRNQKH 112  
  
QY 127 LGESLGNLFKELKNLESRLKGISRVRSKKHEMLVAEIEYMQKRETELQNDNMYLRSKI 186  
Db :|||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :|||: |||:  
113 VGEDESLNNKELQNLQLEHQLDSALKHIRSKNQLMHESVTLQKQDRALQEQNNLSKKV 172  
  
QY 187 TERTG--LQQ---QESSVIHQGT-VYESGVTSSSHQSGQYNNYIAVNLLPEPNQSSNQ 238  
Db :|||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :|||: |||:  
173 KEREKEVAQONQNDQONHNSSTFVLPOOLDSPLHGEAYQNTNVVDNVEGEGNSSQQ 231

RESULT 14  
AGL2\_ARATH  
ID AGL2\_ARATH STANDARD; PRT; 248 AA.  
AC P29382;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Agamous-like MADS box protein AGL2.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX   NCBI_TaxID=3702;
RN   [1]
RP   MEDLINE=91160981; PubMed=1672119;
RA   Ma H., Yanofsky M.F., Meyerowitz E.M.;
RT   "AGL1-AGL6, an Arabidopsis gene family with similarity to floral
RT   homeotic and transcription factor genes.";
RL   Genes Dev. 5:484-495(1991).
CC   -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- DEVELOPMENTAL STAGE: EXPRESSED EARLY DURING FLOWER DEVELOPMENT.
CC   -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC   FACTORS.
CC   -!- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
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CC   or send an email to license@isb-sib.ch).
CC   -----
DR   EMBL; M55551; AAA32732.1; -.
DR   PIR; B39534; B39534.
DR   HSSP; P11746; IMNM.
DR   TRANSFAC; T03024; -.
DR   InterPro; IPR002487; TF_Kbox.
DR   InterPro; IPR002100; TF_MADSbox.
DR   Pfam; PF00319; SRF-TF; 1.
DR   Pfam; PF01486; K-box; 1.
DR   PRINTS; PR00404; MADSDOMAIN.
DR   SMART; SM00432; MADS; 1.
DR   PROSITE; PS00350; MADS_BOX_1; 1.
DR   PROSITE; PS50066; MADS_BOX_2; 1.
KW   Transcription regulation; DNA-binding; Nuclear protein.
FT   DOMAIN 3 57 MADS.
FT   DOMAIN 97 169 K-BOX.
FT   SEQUENCE 248 AA; 28454 MW; 8B70DD4512AC906B CRC64;
SQ
Query Match 32.4%; Score 402.5; DB 1; Length 248;
Best Local Similarity 42.1%; Pred. No. 2.2e-21;
Matches 98; Conservative 38; Mismatches 78; Indels 19; Gaps 6;

Qy 16 IGRGKIEIKRIENTNRQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLYEYANN 75
Db 1 MGRGRVELKRIENKINQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLYEYFCSS 60

Qy 76 S-VRGTIERYKKAC--SDAVNPPTITEANTQYQOQASKRLRRQIRDIQNLRHILGESLG 132
Db 61 SNWLKTLDRYQKCSYGSIEVNNKPAKELENSY--REYLLKGRYENLQROQNLIGEDLG 118

Qy 133 SLNFKELKNLESRLKGISRVRSKKHEMLVAIEYMQKRETELQNDNMVLRSKITERTGL 192
Db 119 PLNSKELEQLERQLDGLSKQVRSIKTYQMLDQLSDLQNKQEQMLLETNRALAMKLDMMIGV 178

Qy 193 QQQESSVIHQGVYESVTSQSHSQGYNNRYIAVNLLPNNSSNQDQPPLQL 245
Db 179 RSHHMGWEGG---EQNVYAHHQASQGLY---QPLECN-----PTLQM 217

RESULT 15
AGL9_LYCES
ID AGL9_LYCES STANDARD; PRT; 224 AA.
AC Q42464;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Agamous-like MADS box protein AGL9 homolog (TM5).
GN TDR5.
OS Lycopersicon esculentum (Tomato).
```

```
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX   NCBI_TaxID=4081;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv.VFNT Cherry; TISSUE=Flower;
RX   MEDLINE=93251098; PubMed=1688249;
RA   Pnueli L., Abu-Abeid M., Zamir D., Nacken W., Schwarz-Sommer Z.,
RA   Lifschitz E.;
RT   "The MADS box gene family in tomato: temporal expression during
RT   floral development, conserved secondary structures and homology with
RT   homeotic genes from Antirrhinum and Arabidopsis.";
RL   Plant J. 1:255-266(1991).
CC   -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR ACTIVE IN INFLORESCENCE
CC   DEVELOPMENT AND FLORAL ORGANOGENESIS (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC   -!- TISSUE SPECIFICITY: FLOWER-SPECIFIC.
CC   -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC   FACTORS.
CC   -!- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
CC   -----
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CC   -----
DR   EMBL; X60758; CAA43170.1; -.
DR   EMBL; X60480; CAA43010.1; -.
DR   HSSP; P11746; IMNM.
DR   TRANSFAC; T03187; -.
DR   InterPro; IPR002487; TF_Kbox.
DR   InterPro; IPR002100; TF_MADSbox.
DR   Pfam; PF00319; SRF-TF; 1.
DR   Pfam; PF01486; K-box; 1.
DR   PRINTS; PR00404; MADSDOMAIN.
DR   SMART; SM00432; MADS; 1.
DR   PROSITE; PS00350; MADS_BOX_1; 1.
DR   PROSITE; PS50066; MADS_BOX_2; 1.
KW   Transcription regulation; DNA-binding; Nuclear protein.
FT   DOMAIN 3 57 MADS.
FT   DOMAIN 98 170 K-BOX.
FT   SEQUENCE 224 AA; 25999 MW; 51D10D30867D06F7 CRC64;
SQ
Query Match 32.3%; Score 401; DB 1; Length 224;
Best Local Similarity 46.5%; Pred. No. 2.5e-21;
Matches 87; Conservative 41; Mismatches 55; Indels 4; Gaps 3;

Qy 16 IGRGKIEIKRIENTNRQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLYEY-AN 74
Db 1 MGRGRVELKRIEGKINQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLYEFCSS 60

Qy 75 NSVRGTIERYKKACSDAVNPPTIT--EANTQYQOQASKRLRRQIRDIQNLRHILGESLG 132
Db 61 SSMLKTLERYQK-CNVGAPEPNISTREALEISSQOQYLLKGRYEALQRSQNLIGEDLG 119

Qy 133 SLNFKELKNLESRLKGISRVRSKKHEMLVAIEYMQKRETELQNDNMVLRSKITERTGL 192
Db 120 PLNSKELESLESLERQLDMSLKOIRSTRQQLMDQLDQTDYQKHEALNEANRTLKQRLMEGSQL 179

Qy 193 QQQESSV 199
Db 180 NLQCSQM 186

Search completed: January 27, 2003, 12:44:41
Job time : 9.96356 secs
```



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OM protein - protein search, using sw model

Run on: January 27, 2003, 12:42:53 ; Search time 14.4413 Seconds  
(without alignments)  
1637.600 Million cell updates/sec

Title: US-09-978-382A-6  
Perfect score: 1242  
Sequence: 1 MEGGASNEVAESSKIGRK.....NLLEPNQNSSNQDPPPLQLV 246

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID       | Description        |
|------------|-------|---------------|--------|----------|--------------------|
| 1          | 1242  | 100.0         | 246    | 2 E39534 | floral homeotic pr |
| 2          | 1238  | 99.7          | 258    | 2 G84858 | floral homeodomain |
| 3          | 1050  | 84.5          | 248    | 2 A39534 | floral homeotic pr |
| 4          | 780.5 | 62.8          | 248    | 2 T03592 | floral homeotic pr |
| 5          | 771   | 62.1          | 247    | 2 S60307 | fbp6 protein - gar |
| 6          | 770.5 | 62.0          | 248    | 2 T07185 | floral homeotic pr |
| 7          | 767.5 | 61.8          | 242    | 2 JQ2212 | pMADS3 protein - g |
| 8          | 742.5 | 59.8          | 239    | 2 A44343 | promotes sex organ |
| 9          | 714.5 | 57.5          | 284    | 2 T05033 | floral homeotic pr |
| 10         | 714.5 | 57.5          | 284    | 2 A85214 | floral homeotic pr |
| 11         | 710.5 | 57.2          | 252    | 2 A43484 | probable transcrip |
| 12         | 710   | 57.2          | 229    | 2 T08040 | MADS-box protein - |
| 13         | 709   | 57.1          | 262    | 2 T08039 | MADS-box protein - |
| 14         | 705.5 | 56.8          | 254    | 2 T01815 | MADS-box protein C |
| 15         | 704.5 | 56.7          | 230    | 2 T04000 | MADS-box protein A |
| 16         | 700.5 | 56.4          | 236    | 2 S59480 | MADS-box protein 3 |
| 17         | 695.5 | 56.0          | 253    | 2 S57586 | MADS-box regulator |
| 18         | 656   | 52.8          | 259    | 2 JQ2289 | hypothetical prote |
| 19         | 647   | 52.1          | 286    | 2 S1934  | floral homeotic pr |
| 20         | 646.5 | 52.1          | 222    | 2 S1934  | MADS-box protein d |
| 21         | 629.5 | 50.7          | 265    | 2 T02261 | MADS-box protein - |
| 22         | 587   | 47.3          | 258    | 2 P00770 | floral homeotic pr |
| 23         | 481   | 38.7          | 261    | 2 S1935  | probable MADS-box  |
| 24         | 479   | 38.6          | 261    | 2 T09603 | MADS-box protein 3 |
| 25         | 451.5 | 36.4          | 242    | 2 T10486 | MADS box protein - |
| 26         | 449.5 | 36.2          | 242    | 2 T09571 | MADS box protein M |
| 27         | 448.5 | 36.1          | 250    | 2 T04167 | MADS box protein - |
| 28         | 443   | 35.7          | 255    | 2 T03408 | MADS box protein - |
| 29         | 436   | 35.1          | 255    | 2 T03398 | MADS box protein - |

|    |       |      |     |          |                    |
|----|-------|------|-----|----------|--------------------|
| 30 | 427   | 34.4 | 252 | 2 F39534 | floral homeotic pr |
| 31 | 421   | 33.9 | 273 | 2 T03410 | MADS box protein - |
| 32 | 420   | 33.8 | 219 | 2 S46526 | MADS box protein m |
| 33 | 418   | 33.7 | 221 | 2 T10751 | MADS-box protein M |
| 34 | 417.5 | 33.6 | 245 | 2 T09569 | MADS box protein M |
| 35 | 415.5 | 33.5 | 213 | 2 T10422 | MADS box protein A |
| 36 | 411   | 33.1 | 214 | 2 T00879 | MADS-box protein A |
| 37 | 409   | 32.9 | 248 | 2 T04170 | MADS box protein - |
| 38 | 407   | 32.8 | 203 | 2 S51936 | MADS-box protein d |
| 39 | 406   | 32.7 | 224 | 2 JQ1690 | MADS box protein f |
| 40 | 406   | 32.7 | 225 | 2 T04168 | MADS box protein - |
| 41 | 405.5 | 32.6 | 249 | 2 T04307 | M79 protein - rice |
| 42 | 405.5 | 32.6 | 249 | 2 T04335 | MADS box protein - |
| 43 | 405   | 32.6 | 250 | 2 T07100 | MADS box protein h |
| 44 | 405   | 32.6 | 257 | 2 S53306 | MADS box protein M |
| 45 | 404   | 32.5 | 246 | 2 T17023 | MADS box protein 1 |

ALIGNMENTS

RESULT 1

E39534  
floral homeotic protein AGL5 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 24-Sep-1999  
C:Accession: E39534  
R;Ma, H.; Yanofsky, M.F.; Meyerowitz, E.M.  
Genes Dev. 5, 484-495, 1991  
A:Title: AGL1-AGL6, an Arabidopsis gene family with similarity to floral homeotic and  
A:Reference number: A39534; MUID:91160981; PMID:1672119  
A:Accession: E39534  
A:Molecule type: DNA  
A:Residues: 1-246 <MAA>

A:Cross-References: GB:M55553; NID:g166595; PIDN:AAA32735.1; PID:g166596  
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain ho  
C:Keywords: DNA binding; nucleus; transcription regulation  
F:17-72/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 100.0%; Score 1242; DB 2; Length 246;  
Best Local Similarity 100.0%; Pred. No. 3.6e-79;  
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |     |                                                            |     |
|----|-----|------------------------------------------------------------|-----|
| QY | 1   | MEGGASNEVAESSKIGRKIGRIKRIENTTNRQVTFCKRRNGLLKAYELSVLCDAEVAL | 60  |
| Db | 1   | MEGGASNEVAESSKIGRKIGRIKRIENTTNRQVTFCKRRNGLLKAYELSVLCDAEVAL | 60  |
| QY | 61  | VIFSTRGRLEYANNVSRGTIERYKKACSDAVNPPTITTEANTQYYQOEASKLRIRDIO | 120 |
| Db | 61  | VIFSTRGRLEYANNVSRGTIERYKKACSDAVNPPTITTEANTQYYQOEASKLRIRDIO | 120 |
| QY | 121 | NLNRHILGESLGNFKELKNLESRLKLGISRVRSKKHEMLVAEIEYMKREIELQNDNM  | 180 |
| Db | 121 | NLNRHILGESLGNFKELKNLESRLKLGISRVRSKKHEMLVAEIEYMKREIELQNDNM  | 180 |
| QY | 181 | YLRSKITERTGLQOQESSVIHQGTVYESGVTSSHQSQGYNNRYIAVNLLPQNSSNQDQ | 240 |
| Db | 181 | YLRSKITERTGLQOQESSVIHQGTVYESGVTSSHQSQGYNNRYIAVNLLPQNSSNQDQ | 240 |
| QY | 241 | PPLQLV 246                                                 |     |
| Db | 241 | PPLQLV 246                                                 |     |

RESULT 2

G84858  
floral homeodomain transcription factor (AGL5) [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 16-Feb-2001  
C:Accession: G84858  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon,  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter

Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.  
A;Reference number: A84420; MUID:20083487; PMID:10617197  
A;Accession: G84858  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-258 <STO>  
A;Cross-references: GB:AE002093; NID:g4512687; PIDN:AAD21741.1; GSPDB:GN00139  
C;Genetics:  
A;Gene: At2g42830  
A;Map position: 2  
C;Superfamily: transcription factor squa; serum response factor DNA-binding domain homol

Query Match 99.7%; Score 1238; DB 2; Length 258;  
Best Local Similarity 100.0%; Pred. No. 7.2e-79;  
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGGASNEVAESSKKIGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVAL 60  
Db 1 MEGGASNEVAESSKKIGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVAL 60

QY 61 VIFSTRGRLYEYANNVSRGTIERKKACSDAVNPPTITEANTQYYQAEASKLRQIRDQ 120  
Db 61 VIFSTRGRLYEYANNVSRGTIERKKACSDAVNPPTITEANTQYYQAEASKLRQIRDQ 120

QY 121 NLNRHILGESLGNFKELKNLESRLKSGISRVRSKKHMLVAIEYMQKREIELQNDNM 180  
Db 121 NLNRHILGESLGNFKELKNLESRLKSGISRVRSKKHMLVAIEYMQKREIELQNDNM 180

QY 181 YLRSKITERTGLQOQESSVTHQGTVEGVTSSHOSGOYNRNNTAVNLLPEPNQSSNOQ 240  
Db 181 YLRSKITERTGLQOQESSVTHQGTVEGVTSSHOSGOYNRNNTAVNLLPEPNQSSNOQ 240

QY 241 PPLQL 245  
Db 241 PPLQL 245

RESULT 3  
A39534  
floral homeotic protein AGL1 [similarity] - *Arabidopsis thaliana*  
N;Alternate names: agamous-like 1 AGL1; shatterproof 1 SHP1; T20N10.130  
C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 09-Jun-2000  
C;Accession: A39534; T49161  
R;Ma, H.; Yanofsky, M.F.; Meyerowitz, E.M.  
Genes Dev. 5, 484-495, 1991  
A;Title: AGL1-AGL6, an *Arabidopsis* gene family with similarity to floral homeotic and tr  
A;Reference number: A39534; MUID:91160981; PMID:1672119  
A;Accession: A39534  
A;Molecule type: DNA  
A;Residues: 1-248 <MAA>  
A;Cross-references: GB:M55550; NID:g166587; PIDN:AAA32730.1; PID:g166588  
R;D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Rudd, S.; I  
submitted to the Protein Sequence Database, April 2000  
A;Reference number: Z25017  
A;Accession: T49161  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-248 <DAN>  
A;Cross-references: EMBL:AL353032; GSPDB:GN00061; ATSP:T20N10.130  
A;Experimental source: cultivar Columbia; BAC clone T20N10  
C;Genetics:  
A;Gene: ATSP:T20N10.130  
A;Map position: 3  
A;Introns: 76/2; 103/3; 124/2; 157/3; 171/3; 185/3  
C;Superfamily: transcription factor squa; serum response factor DNA-binding domain homol  
C;Keywords: DNA binding; nucleus; transcription regulation  
F;17-72/Domain: serum response factor DNA-binding domain homology <SRE>

Query Match 84.5%; Score 1050; DB 2; Length 248;  
Best Local Similarity 85.5%; Pred. No. 7.5e-66;  
Matches 212; Conservative 12; Mismatches 22; Indels 2; Gaps 1;

QY 1 MEGGASNEVAESSKKIGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVAL 60  
Db 1 MEGGSSHDAESSKKIGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVAL 60

QY 61 VIFSTRGRLYEYANNVSRGTIERKKACSDAVNPPTITEANTQYYQAEASKLRQIRDQ 120  
Db 61 VIFSTRGRLYEYANNVSRGTIERKKACSDAVNPPTITEANTQYYQAEASKLRQIRDQ 120

QY 121 NLNRHILGESLGNFKELKNLESRLKSGISRVRSKKHMLVAIEYMQKREIELQNDNM 180  
Db 121 NSNRHIVGESLGNFKELKNLEGRLEKSGISRVRSKKNELVAIEYMQKREMELOHNNM 180

QY 181 YLRSKITE--RTGLQOQESSVTHQGTVEGVTSSHOSGOYNRNNTAVNLLPEPNQSSNQ 238  
Db 181 YLRAKIAEGARLNPDOQESSVIOGTTVYESGVSHDQSOHYNRNYIPVNLLEPNQFSGQ 240

QY 239 DQPLQLV 246  
Db 241 DQPLQLV 248

RESULT 4  
T03592  
floral homeotic protein NAG1 - common tobacco  
C;Species: *Nicotiana tabacum* (common tobacco)  
C;Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 24-Sep-1999  
C;Accession: T03592  
R;Kempin, S.A.; Mandel, M.A.; Yanofsky, M.F.  
Plant Physiol. 103, 1041-1046, 1993  
A;Title: Conversion of perianth into reproductive organs by ectopic expression of the  
A;Reference number: Z14965; MUID:94120000; PMID:7507355  
A;Accession: T03592  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-248 <KEM>  
A;Cross-references: EMBL:L23925; NID:g431735; PIDN:AAA17033.1; PID:g431736  
A;Experimental source: cultivar Samsun; tissue-type immature stamens  
C;Genetics:  
A;Gene: NAG1  
C;Function:  
A;Description: NAG1 seems to be sufficient to convert perianth into reproductive flori  
C;Superfamily: transcription factor squa; serum response factor DNA-binding domain ho  
C;Keywords: DNA binding; nucleus; transcription regulation  
F;18-73/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 62.8%; Score 780.5; DB 2; Length 248;  
Best Local Similarity 66.9%; Pred. No. 3.7e-47;  
Matches 158; Conservative 34; Mismatches 39; Indels 5; Gaps 3;

QY 14 KKIGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGRLYEYA 73  
Db 15 RKLGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSSRGRLYEYA 74

QY 74 NNSVRGTIERKKACSDAVNPPTITEANTQYYQAEASKLRQIRDQNLNRHILGESLGS 133  
Db 75 NNSVRATIERKKACSDSSNTGTSISEANAQYYQAEASKLRAQIGNLQNRNMLGESLAA 134

QY 134 LNFKEKLNLESRLKSGISRVRSKKHMLVAIEYMQKREIELQNDNMVLRSKI--TERTG 191  
Db 135 LSLRDLKNLEOKIEKISKIRSKNELLFALFAIEYMQKREIDLHNNNQYLAKIAETERAQ 194

QY 192 LQQQESSV-THQGTVEGVTSSHOSGOYNRNNTAVNLLPEPNQSSNQDQPLQLV 246  
Db 195 QQQQQQOMNLMFGSSSYELVPPPHQFD--TRNYLQVNLQTLTNNHYTTRQDQPSQLV 248

RESULT 5  
S60307  
fbp6 protein - garden petunia  
C;Species: *Petunia x hybrida* (garden petunia)  
C;Date: 12-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 24-Sep-1999  
C;Accession: S60307

R;Angenent, G.C.; Franken, J.; Busscher, M.; Colombo, L.; van Tunen, A.J.  
Plant J. 4, 101-112, 1993  
A;Title: Petal and stamen formation in petunia is regulated by the homeotic gene fbpl.  
A;Reference number: S60307; MUID:94035167; PMID:8106081  
A;Accession: S60307  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-247 <ANG>  
A;Cross-references: EMBL:X68675; NID:g396198; PIDN:CAA48635.1; PID:g396199  
C;Superfamily: transcription factor squa; serum response factor DNA-binding domain homol  
F;18-73/Domain: serum response factor DNA-binding domain homology <SRF>  
  
Query Match 62.1%; Score 771.; DB 2; Length 247;  
Best Local Similarity 66.1%; Pred. No. 1.7e-46;  
Matches 158; Conservative 30; Mismatches 51; Indels 0; Gaps 0;  
  
QY 8 EVAESKKIGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRG 67  
Db 9 ESSSSQKSGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSSRG 68  
  
QY 68 RLVEYANNVSRGTIERYKACSDAVNPPTITEANTQYYQOEASKLRRQIRDIONLNRHIL 127  
Db 69 RLVEYANNVSRATIDRYKKHADSTSTGVSSEANTQYYQOEAAKLRRQIRDIOQYNRQIV 128  
  
QY 128 GESLGNLKKELKNLESRLKGISRVRSKKHEMLVAEIEYMQKREIEIQNDNMVLRSKIT 187  
Db 129 GEALSSLSRGLKNLEKLEKAGRVRSKKNELLFSEIELMQKREIEMQNANMYLRAKIA 188  
  
QY 188 ERTGLOQESSVIHQGTYESGVTSSHQSGQYNNRYIAVNLLEPNQNSNQDQPPQLQV 246  
Db 189 EVERATOQMNLMHGGSEVQQPMSSTSQPYDARNFLPNLLEPNPHYSRQDQTALQV 247  
  
RESULT 6  
T07185  
floral homeotic protein TAG1 - tomato  
C;Species: Lycopersicon esculentum (tomato)  
C;Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 11-May-2000  
C;Accession: T07185  
R;Pneuli, L.; Hareven, D.; Rounsley, S.D.; Yanofsky, M.F.; Lifschitz, E.  
Plant Cell 6, 163-173, 1994  
A;Title: Isolation of the tomato AGAMOUS gene, TAG1, and analyses of its homeotic role  
A;Reference number: Z15981; MUID:94198593; PMID:7908549  
A;Accession: T07185  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-248 <PNE>  
A;Cross-references: EMBL:L26295; NID:g457381; PIDN:AAA34197.1; PID:g457382  
A;Experimental source: strain VF36; mature pistils  
C;Genetics:  
A;Gene: AGAMOUS; TAG1  
C;Superfamily: transcription factor squa; serum response factor DNA-binding domain homol  
C;Keywords: DNA binding; nucleus; transcription regulation  
F;18-73/Domain: serum response factor DNA-binding domain homology <SRF>  
  
Query Match 62.0%; Score 770.5; DB 2; Length 248;  
Best Local Similarity 64.4%; Pred. No. 1.8e-46;  
Matches 154; Conservative 33; Mismatches 41; Indels 11; Gaps 3;  
  
QY 14 KKIGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGRLEYA 73  
Db 15 RKLGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALVVFSTRGRLEYA 74  
  
QY 74 NNSVRGTIERYKACSDAVNPPTITEANTQYYQOEASKLRRQIRDIONLNRHILGESLGS 133  
Db 75 NNSVKATIERYKACSDSSNTGSEANAQYYQOEASKLRAQIGNLNMNQRNMGEALAG 134  
  
QY 134 LNFKEKLNLESRLKGISRVRSKKHEMLVAEIEYMQKREIEIQNDNMVLRSKITERGLQ 193  
Db 135 MKLKEKLNLEORIEKIGSKIRSKKNELLFAEIEYMQKREVDLHNNNQYLRAKIAETERAQ 194  
  
QY 194 QOESSVIHQGTYESGVTSSHQSGQYNNRYIAVNLLEPNQNSNQDQPPQLQV 246  
Db 195 GRLYEVANNVSRGTIERYKACSDAVNPPTITEANTQYYQOEASKLRRQIRDIONLNRHI 126

Db 195 HQ-----HQQMNLMPGSSSYHELVPVPQFQDTRNYLQVNGLQTNHHYPQDQPPQLV 248  
  
RESULT 7  
JQ2212  
pMADS3 protein - garden petunia  
C;Species: Petunia x hybrida (garden petunia)  
C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 24-Sep-1999  
C;Accession: JQ2212; S34141  
R;Tsuchimoto, S.; van der Krol, A.R.; Chua, N.H.  
Plant Cell 5, 843-853, 1993  
A;Title: Ectopic expression of pMADS3 in transgenic petunia phenocopies the petunia b  
A;Reference number: JQ2212; MUID:94004017; PMID:8104573  
A;Accession: JQ2212  
A;Molecule type: mRNA  
A;Residues: 1-242 <TSU>  
A;Cross-references: EMBL:X72912; NID:g313112; PIDN:CAA51417.1; PID:g313113  
A;Experimental source: floral bud, strain W115  
A;Note: the authors translated codon ATT for residue 174 as Leu  
A;Note: This protein shows high sequence homology to the Arabidopsis AGAMOUS and Anti  
C;Comment: This protein is involved in stamen and carpel development.  
C;Superfamily: transcription factor squa; serum response factor DNA-binding domain ho  
F;18-73/Domain: serum response factor DNA-binding domain homology <SRF>  
  
Query Match 61.8%; Score 767.5; DB 2; Length 242;  
Best Local Similarity 65.7%; Pred. No. 2.8e-46;  
Matches 153; Conservative 36; Mismatches 39; Indels 5; Gaps 3;  
  
QY 14 KKIGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGRLEYA 73  
Db 15 RKLGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSSRGLEYA 74  
  
QY 74 NNSVRGTIERYKACSDAVNPPTITEANTQYYQOEASKLRRQIRDIONLNRHILGESLGS 133  
Db 75 NNSVKATIERYKACSDSSNTGSEANAQYYQOEASKLRAQIGNLNMNQRNFGESLAA 134  
  
QY 134 LNFKEKLNLESRLKGISRVRSKKHEMLVAEIEYMQKREIEIQNDNMVLRSKITERGLQ 193  
Db 135 LNLRLNLEQKIEKGISKIRAKKNELLFAEIEYMQKREIDLHNNNQYLRAKIAETE--R 192  
  
QY 194 QOESSVIHQGTYESGVTSSHQSGQYNNRYIAVNLLEPNQNSNQDQPPQLV 246  
Db 193 SQQMNLMPGSSSYD--LVPPQOSFD-ARNYLOVNGLQTNHHYPQDQPPQLV 242  
  
RESULT 8  
A44343  
promotes sex organ development protein ple - garden snapdragon  
C;Species: Antirrhinum majus (garden snapdragon)  
C;Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 16-Jul-1999  
C;Accession: A44343  
R;Bradley, D.; Carpenter, R.; Sommer, H.; Hartley, N.; Coen, E.  
Cell 72, 85-95, 1993  
A;Title: Complementary floral homeotic phenotypes result from opposite orientations o  
A;Reference number: A44343; MUID:93137332; PMID:8093684  
A;Accession: A44343  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-239 <BRA>  
A;Cross-references: GB:S53900; NID:g264222; PIDN:AAB25101.1; PID:g264223  
A;Note: sequence extracted from NCBI backbone (NCBIP:123356)  
C;Superfamily: transcription factor squa; serum response factor DNA-binding domain ho  
F;15-70/Domain: serum response factor DNA-binding domain homology <SRF>  
  
Query Match 59.8%; Score 742.5; DB 2; Length 239;  
Best Local Similarity 63.1%; Pred. No. 1.5e-44;  
Matches 152; Conservative 38; Mismatches 44; Indels 7; Gaps 3;  
  
QY 7 NEVAESSKKIGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTR 66  
Db 5 NQDSLSLRKNGRGKIEIKRIENITNRQVTFCKRRNGLLKKAYELSVLCDAEVALVVFSSR 64  
  
QY 67 GRLYEVANNVSRGTIERYKACSDAVNPPTITEANTQYYQOEASKLRRQIRDIONLNRHI 126

Db 65 GRLEYANNSVRATIERYKKASADSSNSVSTSEANTQFYQOEANKLRQIREIQTSNRQM 124  
Qy 127 LGESGLSNFKELKNLESRLKGISRVRSKKHEMLVAEIEYMQKREIEQLQNDNMVLRSKI 186  
Db 125 LGEVSNMALKDLKSTAEKVEKAISRIRSKKNELLFAEIEHMQKRELELHNANMFLRAKI 184  
Qy 187 TERTGLQOQESSVIHQGTVYESGVTSSSHQSGQYNNRYIAVNLLEPNQNS-SNQDQPPPLQL 245  
Db 185 AEGERAQQMN--LMPGSDYQPMTSOSYDV----RNFLPNLMPEPNQOQYSRHDQTALQL 238  
Qy 246 V 246  
Db 239 V 239  
RESULT 9  
T05033  
floral homeotic protein agamous - Arabidopsis thaliana (fragment)  
N:Alternate names: probable transcription factor agamous; protein F13C5.130  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 20-Jun-2000  
C:Accession: T05033; S10933  
R:Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schuel  
submitted to the Protein Sequence Database, February 1998  
A:Reference number: Z15395  
A:Accession: T05033  
A:Molecule type: DNA  
A:Residues: 1-284 <BEV>  
A:Cross-references: EMBL:AL021711  
A:Experimental source: cultivar Columbia; BAC clone F13C5  
R:Yanofsky, M.F.; Ma, H.; Bowman, J.L.; Drews, G.N.; Feldmann, K.A.; Meyerowitz, E.M.  
Nature 346, 35-39, 1990  
A:Title: The protein encoded by the Arabidopsis homeotic gene agamous resembles transcri  
A:Reference number: S10933; MUID:90309968; PMID:1973265  
A:Accession: S10933  
A:Molecule type: mRNA  
A:Residues: 'H',1-284 <YAN>  
A:Cross-references: EMBL:X53579; NID:gl6155; PIDN:CAA37642.1; PID:gl345505  
A:Note: DNA sequencing was also done  
C:Genetics:  
A:Gene: agamous  
A:Map position: 4  
A:Note: intron positions not resolved  
A:Note: F13C5.130  
C:Function:  
A:Description: probably involved in regulating genes that determine stamen and carpel de  
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol  
C:Keywords: DNA binding; nucleus; transcription factor; transcription regulation  
F:50-105/Domain: serum response factor DNA-binding domain homology <SRF>  
Query Match 57.5%; Score 714.5; DB 2; Length 284;  
Best Local Similarity 59.2%; Pred. No. 1.6e-42;  
Matches 148; Conservative 38; Mismatches 53; Indels 11; Gaps 4;  
Qy 3 GGASNEVAESSKKIGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVCDAEVALVI 62  
Db 40 GGDSSPL----RKSGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVCDAEVALIV 95  
Qy 63 FSTRGRLEYANNRVGTIERYKKACSDAVNPPTITEANTQYQQEASKLRQIRDIONL 122  
Db 96 FSSRGRLEYSNSVKGTIERYKKAISDNTSGVAEINAQYQQESAKLRQIIISIQNS 155  
Qy 123 NRHILGESLGNLFKELKNLESRLKGISRVRSKKHEMLVAEIEYMQKREIEQLQNDNMVL 182  
Db 156 NRQLMGETIGSMSPKELRNLEGRLESIIRIRSKKNELLFSEIDYMQKREVLDHNDNQIL 215  
Qy 183 RSKITERTGLQOQESSVIHQGTVYESGVTSSSHQSGQ--YNNRYIAVNLLEPN----QNSS 236  
Db 216 RAKIAENE--RNNPSISLMPGGSNYEQLMPPPTQSQPFDSRNYFQVAALQPNHHYSSAG 274  
Qy 237 NQDQPPPLQLV 246  
Db 275 RQDQTALQLV 284  
RESULT 11  
A43484  
probable transcription factor BAG1 - rape  
C:Species: Brassica napus (rape)  
C:Date: 10-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 24-Sep-1999  
C:Accession: A43484  
R:Mandel, M.A.; Bowman, J.L.; Kempin, S.A.; Ma, H.; Meyerowitz, E.M.; Yanofsky, M.F.  
Cell 71, 133-143, 1992  
A:Title: Manipulation of flower structure in transgenic tobacco.  
A:Reference number: A43484; MUID:93008236; PMID:1356631  
A:Accession: A43484  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-252 <MAN>  
A:Cross-references: GB:M99415; NID:gl67125; PIDN:AAA32985.1; PID:gl67126  
A:Note: sequence extracted from NCBI backbone (NCBIP:115468)  
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain ho  
C:Keywords: DNA binding; nucleus; transcription regulation  
F:18-73/Domain: serum response factor DNA-binding domain homology <SRF>  
Query Match 57.2%; Score 710.5; DB 2; Length 252;  
Best Local Similarity 58.4%; Pred. No. 2.7e-42;  
Matches 146; Conservative 39; Mismatches 54; Indels 11; Gaps 4;  
Qy 3 GGASNEVAESSKKIGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVCDAEVALVI 62

Db 65 GRLEYANNSVRATIERYKKASADSSNSVSTSEANTQFYQOEANKLRQIREIQTSNRQM 124  
Qy 127 LGESGLSNFKELKNLESRLKGISRVRSKKHEMLVAEIEYMQKREIEQLQNDNMVLRSKI 186  
Db 125 LGEVSNMALKDLKSTAEKVEKAISRIRSKKNELLFAEIEHMQKRELELHNANMFLRAKI 184  
Qy 187 TERTGLQOQESSVIHQGTVYESGVTSSSHQSGQYNNRYIAVNLLEPNQNS-SNQDQPPPLQL 245  
Db 185 AEGERAQQMN--LMPGSDYQPMTSOSYDV----RNFLPNLMPEPNQOQYSRHDQTALQL 238  
Qy 246 V 246  
Db 239 V 239  
RESULT 9  
T05033  
floral homeotic protein agamous - Arabidopsis thaliana (fragment)  
N:Alternate names: probable transcription factor agamous; protein F13C5.130  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 20-Jun-2000  
C:Accession: T05033; S10933  
R:Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schuel  
submitted to the Protein Sequence Database, February 1998  
A:Reference number: Z15395  
A:Accession: T05033  
A:Molecule type: DNA  
A:Residues: 1-284 <BEV>  
A:Cross-references: EMBL:AL021711  
A:Experimental source: cultivar Columbia; BAC clone F13C5  
R:Yanofsky, M.F.; Ma, H.; Bowman, J.L.; Drews, G.N.; Feldmann, K.A.; Meyerowitz, E.M.  
Nature 346, 35-39, 1990  
A:Title: The protein encoded by the Arabidopsis homeotic gene agamous resembles transcri  
A:Reference number: S10933; MUID:90309968; PMID:1973265  
A:Accession: S10933  
A:Molecule type: mRNA  
A:Residues: 'H',1-284 <YAN>  
A:Cross-references: EMBL:X53579; NID:gl6155; PIDN:CAA37642.1; PID:gl345505  
A:Note: DNA sequencing was also done  
C:Genetics:  
A:Gene: agamous  
A:Map position: 4  
A:Note: intron positions not resolved  
A:Note: F13C5.130  
C:Function:  
A:Description: probably involved in regulating genes that determine stamen and carpel de  
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol  
C:Keywords: DNA binding; nucleus; transcription factor; transcription regulation  
F:50-105/Domain: serum response factor DNA-binding domain homology <SRF>  
Query Match 57.5%; Score 714.5; DB 2; Length 284;  
Best Local Similarity 59.2%; Pred. No. 1.6e-42;  
Matches 148; Conservative 38; Mismatches 53; Indels 11; Gaps 4;  
Qy 3 GGASNEVAESSKKIGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVCDAEVALVI 62  
Db 40 GGDSSPL----RKSGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVCDAEVALIV 95  
Qy 63 FSTRGRLEYANNRVGTIERYKKACSDAVNPPTITEANTQYQQEASKLRQIRDIONL 122  
Db 96 FSSRGRLEYSNSVKGTIERYKKAISDNTSGVAEINAQYQQESAKLRQIIISIQNS 155  
Qy 123 NRHILGESLGNLFKELKNLESRLKGISRVRSKKHEMLVAEIEYMQKREIEQLQNDNMVL 182  
Db 156 NRQLMGETIGSMSPKELRNLEGRLESIIRIRSKKNELLFSEIDYMQKREVLDHNDNQIL 215  
Qy 183 RSKITERTGLQOQESSVIHQGTVYESGVTSSSHQSGQ--YNNRYIAVNLLEPN----QNSS 236  
Db 216 RAKIAENE--RNNPSISLMPGGSNYEQLMPPPTQSQPFDSRNYFQVAALQPNHHYSSAG 274  
Qy 237 NQDQPPPLQLV 246  
Db 275 RQDQTALQLV 284  
RESULT 11  
A43484  
probable transcription factor BAG1 - rape  
C:Species: Brassica napus (rape)  
C:Date: 10-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 24-Sep-1999  
C:Accession: A43484  
R:Mandel, M.A.; Bowman, J.L.; Kempin, S.A.; Ma, H.; Meyerowitz, E.M.; Yanofsky, M.F.  
Cell 71, 133-143, 1992  
A:Title: Manipulation of flower structure in transgenic tobacco.  
A:Reference number: A43484; MUID:93008236; PMID:1356631  
A:Accession: A43484  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-252 <MAN>  
A:Cross-references: GB:M99415; NID:gl67125; PIDN:AAA32985.1; PID:gl67126  
A:Note: sequence extracted from NCBI backbone (NCBIP:115468)  
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain ho  
C:Keywords: DNA binding; nucleus; transcription regulation  
F:18-73/Domain: serum response factor DNA-binding domain homology <SRF>  
Query Match 57.2%; Score 710.5; DB 2; Length 252;  
Best Local Similarity 58.4%; Pred. No. 2.7e-42;  
Matches 146; Conservative 39; Mismatches 54; Indels 11; Gaps 4;  
Qy 3 GGASNEVAESSKKIGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVCDAEVALVI 62

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Db      8 G G E S S - - - - P Q R K A G R G K I E I K R I E N T T N R Q V T F C K R R N G L L K K A Y E L S V L C D A E A L I V 63
QY      63 F S T R G R L Y E Y A N N S V R G T T E R Y K K A C S D A V N P P T I T E A N T Q Y Y Q Q E A S K L R R Q I R D I Q N L 122
Db      64 F S S R G R L Y E Y S N N S V K G T T E R Y K K A I S D N S T G S V A E I N A Q Y Y Q E S A K L R Q Q I I S I Q N S 123
QY      123 N R H I L G E S G L S N F K E L K N L E S R L E K G I S R V R S K K H E M L V A E I Y M Q K R E I E L Q N D N M Y L 182
Db      124 N R Q L M G E T T G S M P K E L N R L E G L D R S V N R I R S K K N E L L F A E I D Y M Q K R E V D L H N D N Q L L 183
QY      183 R S K I T E R T C L Q Q E S S V I H Q G T V Y E S G V T S S H Q S G Q - - Y N R N Y I A V N L L E P N - - - - Q N S S 236
Db      184 R A K I A E N E - R N N F S M L M P G G S N Y E Q I M P P P Q T Q P P D S R N Y F Q V A A L Q P N N H Y S S A G 242
QY      237 N Q D Q P P L Q L V 246
Db      243 R E D Q T A L Q L V 252

RESULT 12
T08040
MADS-box protein - cucumber
C:Species: Cucumis sativus (cucumber)
C:Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 08-Oct-1999
C:Accession: T08040
R:Kater, M.M.; Colombo, L.; Franken, J.; Busscher, M.; Masiero, S.; van Lookeren Campagne
Plant Cell 10, 171-182, 1998
A:Title: Multiple AGAMOUS homologs from cucumber and petunia differ in their ability to
A:Reference number: Z16308; MUID:98158685; PMID:9490741
A:Accession: T08040
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-229 <KAT>
A:Cross-references: EMBL:AF035439; NID:g2997614; PIDN:AAC08529.1; PID:g2997615
C:Genetics:
A:Gene: CUM10
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C:Keywords: DNA binding
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 57.2%; Score 710; DB 2; Length 229;
Best Local Similarity 59.9%; Pred. No. 2.6e-42;
Matches 145; Conservative 41; Mismatches 30; Indels 26; Gaps 4;

QY      16 I G R G K I E I K R I E N T T N R Q V T F C K R R N G L L K K A Y E L S V L C D A E A L I V F S T R G R L Y E Y A N N 75
Db      1 M G R G K I E I K R I E N T T N R Q V T F C K R R N G L L K K A Y E L S V L C D A E A L I V F S S R G R L Y E Y S N N 60

QY      76 S V R G T I E R Y K K A C S D A V N P P T I T E A N T Q Y Y Q Q E A S K L R R Q I R D I Q N L N - - - - R H I L G E S L 131
Db      61 S I K T T I E R Y K K A C S D S S A T S S V T E L N T Q Y Y Q Q E S A K L R Q Q I Q M L Q N S N L V R H L M G D S L 120

QY      132 G S L N F K E L K N L E S R L E K G I S R V R S K K H E M L V A E I Y M Q K R E I L Q N D N M Y L R S K I T E R T G 191
Db      121 S A L T V K E L Q L E N R L E R I T R I R S K K H E M L L A E I Y L O K R E I L E N E N V C I R T K I A E V E R 180

QY      192 L Q Q - - - - - Q E S S V I H Q G T V Y E S G V T S S H Q S G Q Y N R N Y I A V N L L E P - - N Q N S S N Q D Q P P L 243
Db      181 V Q A N M Y S G G Q E L N A I - - - - - Q A L A N S R N F F S P N I M E P A G P V S Y S H Q D K K M L 226

QY      244 Q L 245
Db      227 H L 228

RESULT 13
T08039
MADS-box protein - cucumber
C:Species: Cucumis sativus (cucumber)
C:Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 08-Oct-1999
C:Accession: T08039
R:Kater, M.M.; Colombo, L.; Franken, J.; Busscher, M.; Masiero, S.; van Lookeren Campagne

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Plant Cell 10, 171-182, 1998
A:Title: Multiple AGAMOUS homologs from cucumber and petunia differ in their ability
A:Reference number: Z16308; MUID:98158685; PMID:9490741
A:Accession: T08039
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-262 <KAT>
A:Cross-references: EMBL:AF035438; NID:g2997612; PIDN:AAC08528.1; PID:g2997613
C:Genetics:
A:Gene: CUM1
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain ho
C:Keywords: DNA binding; nucleus; transcription regulation
F:43-98/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 57.1%; Score 709; DB 2; Length 262;
Best Local Similarity 63.7%; Pred. No. 3.6e-42;
Matches 149; Conservative 32; Mismatches 41; Indels 12; Gaps 3;

QY      14 K K I G R G K I E I K R I E N T T N R Q V T F C K R R N G L L K K A Y E L S V L C D A E A L I V F S T R G R L Y E Y A 73
Db      40 R M G R G K I E I K R I E N T T N R Q V T F C K R R N G L L K K A Y E L S V L C D A E A L I V F S S R G R L Y E Y A 99

QY      74 N N S V R G T I E R Y K K A C S D A V N P P T I T E A N T Q Y Y Q Q E A S K L R R Q I R D I Q N L N R H I L G E S L G S 133
Db      100 N N S V K A T I D R Y K K A S D S S N T G S T S E A N T Q F Y Q E A A K L R V Q I G N L Q N S N R N M L G E S L S S 159

QY      134 L N F K E L K N L E S R L E K G I S R V R S K K H E M L V A E I Y M Q K R E I L Q N D N M Y L R S K I T E R T G L Q 193
Db      160 L T A K D L K G L E T K L E K G I S R I R S K K N E L L F A E I Y M R K R E I D L H N N Q M L R A K I A E - - - - - 214

QY      194 Q Q E S S V I H Q G T V Y E S G V T S S H Q S G Q Y N - R N Y I A V N L L E P N Q N S S N Q D Q P P L Q I V 246
Db      215 - S E R V N N M M G G E F E - - - - - L M Q S H P Y D P R D F F Q V G L Q H N H O Y P R O D N M A L Q L V 262

RESULT 14
T10185
MADS-box protein CUS1 - cucumber
C:Species: Cucumis sativus (cucumber)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
C:Accession: T10185
R:Filipecki, M.K.; Sommer, H.; Malepszy, S.
Plant Sci. 125, 63-74, 1997
A:Title: The MADS-box gene CUS1 is expressed during cucumber somatic embryogenesis.
A:Reference number: Z16982
A:Accession: T10185
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-254 <FIL>
A:Cross-references: EMBL:X97801; NID:g1321796
A:Experimental source: cv. Borszczagowski; developmental stage: somatic embryogenesis
C:Genetics:
A:Gene: cus1
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain ho
C:Keywords: DNA binding; transcription factor; transcription regulation
F:26-81/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 56.8%; Score 705.5; DB 2; Length 254;
Best Local Similarity 61.4%; Pred. No. 6e-42;
Matches 140; Conservative 35; Mismatches 50; Indels 3; Gaps 1;

QY      10 A E S S K K I G R G K I E I K R I E N T T N R Q V T F C K R R N G L L K K A Y E L S V L C D A E A L I V F S T R G R L 69
Db      19 S S S S R T G R G K I E I K R I E N T T N R Q V T F C K R R N G L L K K A Y E L S V L C D A E A L I V F S S R G R L 78

QY      70 Y E A N N S V R G T I E R Y K K A C S D A V N P P T I T E A N T Q Y Y Q Q E A S K L R R Q I R D I Q N L N R H I L G E 129
Db      79 Y E A N N S V R A T I S R Y K K A Y S D P S T A M T V S E A N T Q F Y Q Q E S A K L R A Q I G N L Q N L N R H L L G E 138

QY      130 S L G S L N F K E L K N L E S R L E K G I S R V R S K K H E M L V A E I Y M Q K R E I L Q N D N M Y L R S K I T E R 189
Db      139 S I S S L S V K D L K S L E V K L E K G I S R I R S K K N E L L F S E I Y M Q K R E I L H T N N Q L I R A K I A E T 198

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QY 190 TGLOQQESSVIHQGVY--ESGVTSSHQSGQYNNRYIAVNLLEPNQN 234  
Db 199 ERSQQTNASNNNGIATRRGEGSGMGTNLENNHHQYDSTNYFDPHN 246

RESULT 15

T04000  
MADS-box protein AGL11 - Arabidopsis thaliana  
N:Alternate names: protein T5L19.90  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 16-Jul-1999  
C:Accession: T04000  
R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.  
submitted to the Protein Sequence Database, March 1999  
A:Reference number: Z15184  
A:Accession: T04000  
A:Molecule type: DNA  
A:Residues: 1-230 <BEV>  
A:Cross-references: EMBL:AL049481  
A:Experimental source: cultivar Columbia; BAC clone T5L19  
C:Genetics:  
A:Gene: AGL11  
A:Map position: 4  
A:Introns: 61/2; 88/3; 109/2; 142/3; 156/3; 170/3  
A:Note: T5L19.90  
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol  
C:Keywords: DNA binding  
F:2-57/Domain: serum response factor DNA-binding domain homology <SRE>

Query Match 56.7%; Score 704.5; DB 2; Length 230;  
Best Local Similarity 62.2%; Pred. No. 6.2e-42;  
Matches 138; Conservative 33; Mismatches 44; Indels 7; Gaps 1;

QY 16 IGRGKIEIKRTENTTRQVTFCKRRGLLKKAYELSVLCDAEVALVIFSTRGRLYEYANN 75  
Db 1 MGRGKIEIKRTENSTNRQVTFCKRRGLLKKAYELSVLCDAEVALVIFSTRGRLYEYANN 60  
QY 76 SVRGTIERYKKACSDAVNPPTITEANTQYQOEASKLRRQIRDIQNLRHILGESLGS LN 135  
Db 61 NIRSTIERYKKACSDSTNTSTVQEIINAAYQQESAKLRQIQTIQNSNRNLMGDSL SLS 120  
QY 136 FXELKNLESRLKGISRVRSKKHEMLVAEIEYMQKREIELQNDNMVLRSKITER TGLQQQ 195  
Db 121 VKELQVENRLEKAISRIRSKHELLLVEIENAAQKREIELDENIYLR TKVAEVERYQQH 180  
QY 196 ESSVIHQGVTVESGVTSSHQSGQYNNRYIAVNLLEPNQNSSN 237  
Db 181 HHQMV-----SGSEINAIELASRNYFAHSIMTAGSGSGN 215

Search completed: January 27, 2003, 12:46:16  
Job time : 15.4413 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2003, 12:44:48 ; Search time 8.46559 seconds  
(without alignments)  
586.365 Million cell updates/sec

Title: US-09-978-382A-6  
Perfect score: 1242  
Sequence: 1 MEGASNEVAESSKKTGRGK.....NLLEPNQSSNQDQPPLQLV 246

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 122226

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA.\*

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- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
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- 14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description      |
|------------|-------|-------------|--------|----|------------------|
| 1          | 1242  | 100.0       | 246    | 9  | US-09-978-729A-6 |
| 2          | 1242  | 100.0       | 246    | 9  | US-09-981-087A-6 |
| 3          | 1242  | 100.0       | 246    | 9  | US-09-978-382A-6 |
| 4          | 1242  | 100.0       | 246    | 9  | US-09-978-740A-6 |
| 5          | 1242  | 100.0       | 246    | 10 | US-09-978-730-6  |
| 6          | 1050  | 84.5        | 248    | 9  | US-09-978-729A-4 |
| 7          | 1050  | 84.5        | 248    | 9  | US-09-981-087A-4 |
| 8          | 1050  | 84.5        | 248    | 9  | US-09-978-382A-4 |
| 9          | 1050  | 84.5        | 248    | 9  | US-09-978-740A-4 |
| 10         | 1050  | 84.5        | 248    | 10 | US-09-978-730-4  |
| 11         | 421   | 33.9        | 273    | 9  | US-09-853-450-8  |
| 12         | 417   | 33.6        | 240    | 10 | US-09-970-624-2  |
| 13         | 411   | 33.1        | 214    | 9  | US-09-853-450-34 |
| 14         | 402.5 | 32.4        | 248    | 9  | US-09-853-450-28 |
| 15         | 397.5 | 32.0        | 251    | 9  | US-09-853-450-12 |
| 16         | 397   | 32.0        | 255    | 9  | US-09-853-450-10 |
| 17         | 389   | 31.3        | 250    | 9  | US-09-853-450-30 |
| 18         | 382   | 30.8        | 256    | 9  | US-09-853-450-2  |
| 19         | 378   | 30.4        | 242    | 9  | US-09-978-729A-2 |

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| 20 | 378   | 30.4 | 242 | 9  | US-09-981-087A-2    |
| 21 | 378   | 30.4 | 242 | 9  | US-09-978-382A-2    |
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| 24 | 378   | 30.4 | 253 | 9  | US-09-853-450-4     |
| 25 | 376   | 30.3 | 255 | 9  | US-09-853-450-6     |
| 26 | 374.5 | 30.2 | 237 | 9  | US-09-853-450-32    |
| 27 | 348.5 | 28.1 | 220 | 9  | US-09-853-450-38    |
| 28 | 336.5 | 27.1 | 150 | 9  | US-09-853-450-14    |
| 29 | 322   | 25.9 | 210 | 9  | US-09-853-450-36    |
| 30 | 268.5 | 21.6 | 173 | 9  | US-09-853-450-40    |
| 31 | 248   | 20.0 | 105 | 10 | US-09-767-215-10    |
| 32 | 244.5 | 19.7 | 192 | 9  | US-09-853-450-50    |
| 33 | 216   | 17.4 | 507 | 10 | US-09-876-187-2     |
| 34 | 216   | 17.4 | 507 | 10 | US-09-749-728B-13   |
| 35 | 213   | 17.1 | 465 | 10 | US-09-749-728B-17   |
| 36 | 213   | 17.1 | 473 | 10 | US-09-876-187-6     |
| 37 | 213   | 17.1 | 473 | 10 | US-09-876-187-8     |
| 38 | 209   | 16.8 | 365 | 10 | US-09-876-187-4     |
| 39 | 209   | 16.8 | 365 | 10 | US-09-749-728B-15   |
| 40 | 202.5 | 16.3 | 521 | 10 | US-09-749-728B-19   |
| 41 | 198.5 | 16.0 | 676 | 10 | US-09-801-368-302   |
| 42 | 197.5 | 15.9 | 286 | 10 | US-09-801-368-188   |
| 43 | 159   | 12.8 | 452 | 10 | US-09-801-368-336   |
| 44 | 97.5  | 7.9  | 374 | 10 | US-09-925-302-711   |
| 45 | 95.5  | 7.7  | 697 | 10 | US-09-815-242-12798 |

## ALIGNMENTS

### RESULT 1

US-09-978-729A-6  
; Sequence 6, Application US/09978729A  
; Patent No. US20020178465A1  
; GENERAL INFORMATION:

; APPLICANT: Yanofsky, Martin F.

; APPLICANT: Liljegren, Sarah

; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 19452A-000950US

; CURRENT APPLICATION NUMBER: US/09/978,729A

; CURRENT FILING DATE: 2002-06-10

; PRIOR APPLICATION NUMBER: US 60/090,649

; PRIOR FILING DATE: 1998-06-25

; PRIOR APPLICATION NUMBER: US 09/339,998

; PRIOR FILING DATE: 1999-06-25

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 6

; LENGTH: 246

; TYPE: PRT

; ORGANISM: Arabidopsis sp.

US-09-978-729A-6

Query Match 100.0%; Score 1242; DB 9; Length 246;  
Best Local Similarity 100.0%; Pred. No. 2.8e-99;  
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| Db | 1   | MEGASNEVAESSKKGKIGRKIEIKRIENTNRQVTFCKRRNGLLKAYELSVLCDAEVAL  | 60  |
| QY | 61  | VIFSTRGRUYEYANNSVRGTIERYKKACSDAVNPPTITEANTQYQOEASKLRRIQDIQ  | 120 |
| Db | 61  | VIFSTRGRUYEYANNSVRGTIERYKKACSDAVNPPTITEANTQYQOEASKLRRIQDIQ  | 120 |
| QY | 121 | NLNRHILGESLGSNFKELKNLESRLKIGISRVRSKKHEMLVAEIEYMQKREIELQNDNM | 180 |
| Db | 121 | NLNRHILGESLGSNFKELKNLESRLKIGISRVRSKKHEMLVAEIEYMQKREIELQNDNM | 180 |
| QY | 181 | YLSKITERGTGLQQOESSVIHQITVYESGVYSSHOSGQYNNRYIAVNLLPQNQSSNQDQ | 240 |



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Db 181 YLRSKITRTGLQQESSVIHQGTVESSVSHQSGQYNNRYIAVNLLEPNQSSNQDQ 240

QY 241 PPLQLV 246
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Db 241 PPLQLV 246

RESULT 2
US-09-981-087A-6
; Sequence 6, Application US/09981087A
; Patent No. US20020178466A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegren, Sarah
; APPLICANT: Farrandiz, Cristina
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-000940US
; CURRENT APPLICATION NUMBER: US/09/981,087A
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-981-087A-6

Query Match 100.0%; Score 1242; DB 9; Length 246;
Best Local Similarity 100.0%; Pred. No. 2.8e-99;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGGASNEVAESSKKIGRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVAL 60
Db 1 MEGGASNEVAESSKKIGRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVAL 60

QY 61 VIFSTRGRLYEYANNVSRGTIERVKKACSDAVNPPTITEANTQYYQOEASKLRROI 120
Db 61 VIFSTRGRLYEYANNVSRGTIERVKKACSDAVNPPTITEANTQYYQOEASKLRROI 120

QY 121 NLNRHILGESLGNFKELKNLESRLKGISRVRSKKHMLVAEIEYMQKREIELQNDNM 180
Db 121 NLNRHILGESLGNFKELKNLESRLKGISRVRSKKHMLVAEIEYMQKREIELQNDNM 180

QY 181 YLRSKITRTGLQQESSVIHQGTVESSVSHQSGQYNNRYIAVNLLEPNQSSNQDQ 240
Db 181 YLRSKITRTGLQQESSVIHQGTVESSVSHQSGQYNNRYIAVNLLEPNQSSNQDQ 240

QY 241 PPLQLV 246
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Db 241 PPLQLV 246

RESULT 3
US-09-978-382A-6
; Sequence 6, Application US/09978382A
; Publication No. US20020194647A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegren, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-000930US
; CURRENT APPLICATION NUMBER: US/09/978,382A
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-978-382A-6

Query Match 100.0%; Score 1242; DB 9; Length 246;
Best Local Similarity 100.0%; Pred. No. 2.8e-99;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGGASNEVAESSKKIGRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVAL 60
Db 1 MEGGASNEVAESSKKIGRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVAL 60

QY 61 VIFSTRGRLYEYANNVSRGTIERVKKACSDAVNPPTITEANTQYYQOEASKLRROI 120
Db 61 VIFSTRGRLYEYANNVSRGTIERVKKACSDAVNPPTITEANTQYYQOEASKLRROI 120

QY 121 NLNRHILGESLGNFKELKNLESRLKGISRVRSKKHMLVAEIEYMQKREIELQNDNM 180
Db 121 NLNRHILGESLGNFKELKNLESRLKGISRVRSKKHMLVAEIEYMQKREIELQNDNM 180

QY 181 YLRSKITRTGLQQESSVIHQGTVESSVSHQSGQYNNRYIAVNLLEPNQSSNQDQ 240
Db 181 YLRSKITRTGLQQESSVIHQGTVESSVSHQSGQYNNRYIAVNLLEPNQSSNQDQ 240

QY 241 PPLQLV 246
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Db 241 PPLQLV 246

RESULT 4
US-09-978-740A-6
; Sequence 6, Application US/09978740A
; Publication No. US20030005481A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegren, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-000960US
; CURRENT APPLICATION NUMBER: US/09/978,740A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-978-740A-6

Query Match 100.0%; Score 1242; DB 9; Length 246;
Best Local Similarity 100.0%; Pred. No. 2.8e-99;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGGASNEVAESSKKIGRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVAL 60
Db 1 MEGGASNEVAESSKKIGRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVAL 60

QY 61 VIFSTRGRLYEYANNVSRGTIERVKKACSDAVNPPTITEANTQYYQOEASKLRROI 120
Db 61 VIFSTRGRLYEYANNVSRGTIERVKKACSDAVNPPTITEANTQYYQOEASKLRROI 120

QY 121 NLNRHILGESLGNFKELKNLESRLKGISRVRSKKHMLVAEIEYMQKREIELQNDNM 180
Db 121 NLNRHILGESLGNFKELKNLESRLKGISRVRSKKHMLVAEIEYMQKREIELQNDNM 180

QY 181 YLRSKITRTGLQQESSVIHQGTVESSVSHQSGQYNNRYIAVNLLEPNQSSNQDQ 240
Db 181 YLRSKITRTGLQQESSVIHQGTVESSVSHQSGQYNNRYIAVNLLEPNQSSNQDQ 240

QY 241 PPLQLV 246
|||||
Db 241 PPLQLV 246
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QY 121 NLNRHILGESLSLNFKEKLNLESRLKLGISRVRSKKHMLVAIEIYMQKRETELQNDNM 180
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Db 121 NLNRHILGESLSLNFKEKLNLESRLKLGISRVRSKKHMLVAIEIYMQKRETELQNDNM 180
|||||
QY 181 YLRSKITERTGLQOQESSVHQGTYYESGVTSQSHQSGQYNNRYIAVNLLPQNSSNQDQ 240
|||||
Db 181 YLRSKITERTGLQOQESSVHQGTYYESGVTSQSHQSGQYNNRYIAVNLLPQNSSNQDQ 240
|||||
QY 241 PPLQLV 246
|||||
Db 241 PPLQLV 246
|||||

RESULT 5
US-09-978-730-6
; Sequence 6, Application US/09978730
; Patent No. US20020129403A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegren, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-000920US
; CURRENT APPLICATION NUMBER: US/09/978,730
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-978-730-6

Query Match 100.0%; Score 1242; DB 10; Length 246;
Best Local Similarity 100.0%; Pred. No. 2.8e-99;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGGASNEVAESSKKIGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVAL 60
|||||
Db 1 MEGGASNEVAESSKKIGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVAL 60
|||||
QY 61 VIFSTRGRLYEYANNVSRGTIERYKKACSDAVNPPTITEANTQYQQEASKLRRIQ 120
|||||
Db 61 VIFSTRGRLYEYANNVSRGTIERYKKACSDAVNPPTITEANTQYQQEASKLRRIQ 120
|||||
QY 121 NLNRHILGESLSLNFKEKLNLESRLKLGISRVRSKKHMLVAIEIYMQKRETELQNDNM 180
|||||
Db 121 NLNRHILGESLSLNFKEKLNLESRLKLGISRVRSKKHMLVAIEIYMQKRETELQNDNM 180
|||||
QY 181 YLRSKITERTGLQOQESSVHQGTYYESGVTSQSHQSGQYNNRYIAVNLLPQNSSNQDQ 240
|||||
Db 181 YLRSKITERTGLQOQESSVHQGTYYESGVTSQSHQSGQYNNRYIAVNLLPQNSSNQDQ 240
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QY 241 PPLQLV 246
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Db 241 PPLQLV 246
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RESULT 6
US-09-978-729A-4
; Sequence 4, Application US/09978729A
; Patent No. US20020178465A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegren, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; TITLE OF INVENTION: Plants
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; FILE REFERENCE: 19452A-000950US
; CURRENT APPLICATION NUMBER: US/09/978,729A
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-978-729A-4

Query Match 84.5%; Score 1050; DB 9; Length 248;
Best Local Similarity 85.5%; Pred. No. 7.7e-83;
Matches 212; Conservative 12; Mismatches 22; Indels 2; Gaps 1;

QY 1 MEGGASNEVAESSKKIGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVAL 60
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Db 1 MEGGASNEVAESSKKIGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVAL 60
|||||
QY 61 VIFSTRGRLYEYANNVSRGTIERYKKACSDAVNPPTITEANTQYQQEASKLRRIQ 120
|||||
Db 61 VIFSTRGRLYEYANNVSRGTIERYKKACSDAVNPPTITEANTQYQQEASKLRRIQ 120
|||||
QY 121 NLNRHILGESLSLNFKEKLNLESRLKLGISRVRSKKHMLVAIEIYMQKRETELQNDNM 180
|||||
Db 121 NSNRHIVGESLSLNFKEKLNLESRLKLGISRVRSKKHMLVAIEIYMQKRETELQNDNM 180
|||||
QY 181 YLRSKITE--RTGLQOQESSVHQGTYYESGVTSQSHQSGQYNNRYIAVNLLPQNSSNQ 238
|||||
Db 181 YLRKIAEGARLNPDOQESSVIOGTTVYESGVSHDQSOHYNRYIPVNLLEPNQOFSQ 240
|||||
QY 239 DQPPLQLV 246
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Db 241 DQPPLQLV 248
|||||

RESULT 7
US-09-981-087A-4
; Sequence 4, Application US/09981087A
; Patent No. US20020178466A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegren, Sarah
; APPLICANT: Farrandiz, Cristina
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-000940US
; CURRENT APPLICATION NUMBER: US/09/981,087A
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-981-087A-4

Query Match 84.5%; Score 1050; DB 9; Length 248;
Best Local Similarity 85.5%; Pred. No. 7.7e-83;
Matches 212; Conservative 12; Mismatches 22; Indels 2; Gaps 1;

QY 1 MEGGASNEVAESSKKIGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVAL 60
|||||
Db 1 MEGGASNEVAESSKKIGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVAL 60
|||||
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QY 61 VIFSTRGRLEYANNVSRGTIERYKKACSDAVNPPTITEANTQYQQEASKLRQIRDQ 120
Db 61 VIFSTRGRLEYANNVSRGTIERYKKACSDAVNPPTITEANTQYQQEASKLRQIRDQ 120
QY 121 NLNRHILGESLGNFKELKNLESRLKGISRVRSKKHEMLVAIEYMQKREIELQNDNM 180
Db 121 NSNRHIVGESLGNFKELKNLEGRLEKGISRVRSKKNELLVAEIYMQKREMLQHNMM 180
QY 181 YLRSKITE--RTGLQQQESSVHOGTVYESGVTSSHQSQYNNRYIAVNLLEPNQNSNQ 238
Db 181 YLRKIAEGARLNPDDQESSVIOGTTVYESGVSSHQSQHYNNRYIPVNLLEPNQQFSQ 240
QY 239 DQPLQLV 246
Db 241 DQPLQLV 248

RESULT 8
US-09-978-382A-4
; Sequence 4, Application US/09978382A
; Publication No. US20020194647A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegen, Sarah
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-000930US
; CURRENT APPLICATION NUMBER: US/09/978,382A
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-978-382A-4

Query Match 84.5%; Score 1050; DB 9; Length 248;
Best Local Similarity 85.5%; Pred. No. 7.7e-83;
Matches 212; Conservative 12; Mismatches 22; Indels 2; Gaps 1;

QY 1 MEGGASNEVAESSKKIGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVAL 60
Db 1 MEEGGSHDAESSKKLGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVAL 60
QY 61 VIFSTRGRLEYANNVSRGTIERYKKACSDAVNPPTITEANTQYQQEASKLRQIRDQ 120
Db 61 VIFSTRGRLEYANNVSRGTIERYKKACSDAVNPPTITEANTQYQQEASKLRQIRDQ 120
QY 121 NLNRHILGESLGNFKELKNLESRLKGISRVRSKKHEMLVAIEYMQKREIELQNDNM 180
Db 121 NSNRHIVGESLGNFKELKNLEGRLEKGISRVRSKKNELLVAEIYMQKREMLQHNMM 180
QY 181 YLRSKITE--RTGLQQQESSVHOGTVYESGVTSSHQSQYNNRYIAVNLLEPNQNSNQ 238
Db 181 YLRKIAEGARLNPDDQESSVIOGTTVYESGVSSHQSQHYNNRYIPVNLLEPNQQFSQ 240
QY 239 DQPLQLV 246
Db 241 DQPLQLV 248

RESULT 9
US-09-978-740A-4
; Sequence 4, Application US/09978740A
; Publication No. US20030005481A1
; GENERAL INFORMATION:
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; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegen, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-000960US
; CURRENT APPLICATION NUMBER: US/09/978,740A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-978-740A-4

Query Match 84.5%; Score 1050; DB 9; Length 248;
Best Local Similarity 85.5%; Pred. No. 7.7e-83;
Matches 212; Conservative 12; Mismatches 22; Indels 2; Gaps 1;

QY 1 MEGGASNEVAESSKKIGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVAL 60
Db 1 MEEGGSHDAESSKKLGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVAL 60
QY 61 VIFSTRGRLEYANNVSRGTIERYKKACSDAVNPPTITEANTQYQQEASKLRQIRDQ 120
Db 61 VIFSTRGRLEYANNVSRGTIERYKKACSDAVNPPTITEANTQYQQEASKLRQIRDQ 120
QY 121 NLNRHILGESLGNFKELKNLESRLKGISRVRSKKHEMLVAIEYMQKREIELQNDNM 180
Db 121 NSNRHIVGESLGNFKELKNLEGRLEKGISRVRSKKNELLVAEIYMQKREMLQHNMM 180
QY 181 YLRSKITE--RTGLQQQESSVHOGTVYESGVTSSHQSQYNNRYIAVNLLEPNQNSNQ 238
Db 181 YLRKIAEGARLNPDDQESSVIOGTTVYESGVSSHQSQHYNNRYIPVNLLEPNQQFSQ 240
QY 239 DQPLQLV 246
Db 241 DQPLQLV 248

RESULT 10
US-09-978-730-4
; Sequence 4, Application US/09978730
; Patent No. US20020129403A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegen, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-000920US
; CURRENT APPLICATION NUMBER: US/09/978,730
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-978-730-4

Query Match 84.5%; Score 1050; DB 10; Length 248;
Best Local Similarity 85.5%; Pred. No. 7.7e-83;
Matches 212; Conservative 12; Mismatches 22; Indels 2; Gaps 1;
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QY 1 MEGGASNEVAESSKIGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVAL 60
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MEGGSSDAESSKGLRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVAL 60
QY 61 VIFSTRGLYEVANNSVGRGTIERKKACSDAVNPPTITEANTQYYQOEASKLRRQIRIO 120
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 VIFSTRGLYEVANNSVGRGTIERKKACSDAVNPPTITEANTQYYQOEASKLRRQIRIO 120
QY 121 NLNRHILGESLGNLFELKNLESRLKGISVRSKKHEMLVAEIEYMQKREIELQNDNM 180
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 NSNRHIVGESLGNLFELKNLESRLKGISVRSKKHEMLVAEIEYMQKREIELQNDNM 180
QY 181 YLRSKITE--RTGLQQOESSVIHQGTYESGVTSSHSGQYNNRYIAVNLLEPNQNSNQ 238
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 YLRAKIAEGARLNPQQOESSVIHQGTYESGVSSHDSQHYNNRYIPVNLLEPNQOFSQ 240
QY 239 DQPLQLV 246
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Db 241 DQPLQLV 248
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## RESULT 11

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US-09-853-450-8
; Sequence 8, Application US/09853450
; Publication No. US20020194645A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Pelaz, Soraya
; APPLICANT: Ditta, Gary
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; TITLE OF INVENTION: Exhibiting Modulated Reproductive Development
; FILE REFERENCE: 19452A-002400US
; CURRENT APPLICATION NUMBER: US/09/853,450
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: APETAL1 (AP1)
US-09-853-450-8
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Query Match 33.9%; Score 421; DB 9; Length 273;
Best Local Similarity 37.3%; Pred. No. 5.9e-29;
Matches 98; Conservative 43; Mismatches 86; Indels 36; Gaps 4;
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QY 16 IGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGLYEVANN 75
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Db 1 MGRGVQLKRIENKINQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGLYEVANN 75
QY 76 SVRGTI----ERYKKACSDAVNPPTITEANTQYYQOEASKLRRQIRIOQLNRHILGESL 131
  | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db 61 SRMDILERYYSYAEKALISAESSEGN---WCHYRKLKAKETIQCKHKLGMEDL 117
QY 132 GSNLFELKNLESRLKGISVRSKKHEMLVAEIEYMQKREIELQNDNMVLRSKITER-- 189
  ||| ||||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db 118 ESLNFKELQLEQQLDSSSLKHRSKSHLMAESISELQKKERSLOENKALQKLAERQK 177
QY 190 ---TGLQQOESSVIHQGTYESGVTSSHQ-----GOYNNR 222
  : |||: | : ||| |
Db 178 AVASRQQQQQQQVQWDDQTHAQATSSSSSFMRRQDQQLPPPHNICFPPLTMGDRGEE 237
QY 223 YIAVNLLEPNQNSNQDQPLQL 245
  | : | |||:
Db 238 LAAAAAAQQQQPLPQQAQPOLRI 260
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## RESULT 12

US-09-970-624-2

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; Sequence 2, Application US/09970624
; Patent No. US20020124284A1
; GENERAL INFORMATION:
; APPLICANT: Bruce, Wesley B.
; TITLE OF INVENTION: A Nitrate-Responsive Root
; TITLE OF INVENTION: Transcriptional Factor
; FILE REFERENCE: 1263
; CURRENT APPLICATION NUMBER: US/09/970,624
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: US 60/238,292
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Zea mays
US-09-970-624-2
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Query Match 33.6%; Score 417; DB 10; Length 240;
Best Local Similarity 38.7%; Pred. No. 1.1e-28;
Matches 96; Conservative 53; Mismatches 73; Indels 26; Gaps 7;
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QY 16 IGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGLYEVANN 75
  :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGRGVIRRIDNSTSRQVTFESKRNGIFPKAKELAILCDAEVLGVLVFSSTRGLYEVSS 60
QY 76 SVRGTIERKKACSD--AVNPPTITEANTQYYQOEASKLRRQIRIOQLNRHILGESL 132
  |:: ||| | | | : || : ::|||: |||: |||: |||: |||: |||:
Db 61 SMKSVIDRYGKAKEEQVYANP-----NSELFWQREASLRQQLHNLQENYRQLTGDDLS 116
QY 133 SLNFKELKNLESRLKGISVRSKKHEMLVAEIEYMQKREIELQNDNMVLRSKITER 192
  || |||:||||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db 117 GLNVKELQLENQLETSLRGVRAKRDHLLEIDHDLNRKASLFHQENTDLYNKI----NL 172
QY 193 QQOESSVIHQGTYES-GVTSSHSGQYNNRYIAVNLLE-----PNQNSNQDQP 241
  :||: ||: |||: | : : | : | : | : | : | : | : | : | : | :
Db 173 IRQENDELHK-KIVETEGSPGVNRESPTPFNFVAVVETRDVPVQLELSTLPQNNIEPSTA 231
QY 242 P---LQLV 246
  | |||:
Db 232 PKLGLQLI 239
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## RESULT 13

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US-09-853-450-34
; Sequence 34, Application US/09853450
; Publication No. US20020194645A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Pelaz, Soraya
; APPLICANT: Ditta, Gary
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; TITLE OF INVENTION: Exhibiting Modulated Reproductive Development
; FILE REFERENCE: 19452A-002400US
; CURRENT APPLICATION NUMBER: US/09/853,450
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: AGL20 (SUPPRESSOR OF CONSTANS (CO) OVEREXPRESSION
; OTHER INFORMATION: 1 (SOC1))
US-09-853-450-34
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Query Match 33.1%; Score 411; DB 9; Length 214;
Best Local Similarity 43.0%; Pred. No. 3.1e-28;
Matches 77; Conservative 51; Mismatches 47; Indels 4; Gaps 1;
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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2003, 12:39:28 ; Search time 31.3725 Seconds  
(without alignments)  
1044.854 Million cell updates/sec

Title: US-09-978-382A-6  
Perfect score: 1242  
Sequence: 1 MEGGASNEVAESSKKTGRGK.....NLLEPNQNSSNQDPPPLQLV 246

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_101002.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID        | Description        |
|------------|-------|-------------|--------|-----------|--------------------|
| 1          | 1242  | 100.0       | 246    | AAW81000  | Arabidopsis AGL5 p |
| 2          | 1238  | 99.7        | 258    | AAAG32583 | Arabidopsis thalia |
| 3          | 1050  | 84.5        | 248    | AAW80999  | Arabidopsis AGL1 p |
| 4          | 1050  | 84.5        | 248    | AAAG09411 | Arabidopsis thalia |
| 5          | 824.5 | 66.4        | 251    | AAAG99633 | Eucalyptus AGE-1 p |
| 6          | 746.5 | 60.1        | 241    | AAAY58656 | Poplar PRAG-1 flor |
| 7          | 746.5 | 60.1        | 241    | AAAB68437 | Amino acid sequenc |
| 8          | 746.5 | 60.1        | 241    | ABG30867  | Poplar floral home |
| 9          | 719.5 | 57.9        | 238    | AAAY58657 | Poplar PRAG-2 flor |
| 10         | 719.5 | 57.9        | 238    | AAAB68438 | Amino acid sequenc |

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|----|-------|------|-----|----|-----------|--------------------|
| 11 | 719.5 | 57.9 | 238 | 23 | ABG30868  | Poplar floral home |
| 12 | 714.5 | 57.5 | 300 | 21 | AAAG52721 | Arabidopsis thalia |
| 13 | 706.5 | 56.9 | 277 | 21 | AAAG16689 | Arabidopsis thalia |
| 14 | 706.5 | 56.9 | 277 | 21 | AAAG40212 | Arabidopsis thalia |
| 15 | 704.5 | 56.7 | 230 | 21 | AAAG16690 | Arabidopsis thalia |
| 16 | 704.5 | 56.7 | 230 | 21 | AAAG40213 | Arabidopsis thalia |
| 17 | 702   | 56.5 | 221 | 21 | AAAY44804 | Petunia hybrida ne |
| 18 | 702   | 56.5 | 221 | 21 | AAAY58648 | Petunia nectary-sp |
| 19 | 698   | 56.2 | 185 | 21 | AAAB32638 | Eucalyptus grandis |
| 20 | 690.5 | 55.6 | 264 | 23 | ABG60988  | Novel floral meris |
| 21 | 680   | 54.8 | 257 | 21 | AAAG33135 | Zea mays protein f |
| 22 | 680   | 54.8 | 260 | 21 | AAAG33134 | Zea mays protein f |
| 23 | 680   | 54.8 | 283 | 21 | AAAG33133 | Zea mays protein f |
| 24 | 676   | 54.4 | 268 | 23 | ABG60931  | Novel floral meris |
| 25 | 673   | 54.2 | 133 | 21 | AAAG07156 | Arabidopsis thalia |
| 26 | 658.5 | 53.0 | 229 | 17 | AAAG9637  | Eucalyptus AGE-2 p |
| 27 | 648.5 | 52.2 | 222 | 21 | AAAB26795 | Plant reproductive |
| 28 | 630   | 50.7 | 268 | 21 | AAAG43856 | Zea mays protein f |
| 29 | 539   | 43.4 | 161 | 21 | AAAB33229 | Eucalyptus grandis |
| 30 | 522   | 42.0 | 122 | 21 | AAAG37576 | Arabidopsis thalia |
| 31 | 503   | 40.5 | 142 | 21 | AAAG12611 | Zea mays protein f |
| 32 | 503   | 40.5 | 155 | 21 | AAAG12609 | Z. mays protein f  |
| 33 | 479   | 38.6 | 261 | 19 | AAW48623  | Pinus radiata cone |
| 34 | 462.5 | 37.2 | 260 | 23 | ABG60946  | Novel floral meris |
| 35 | 449.5 | 36.2 | 181 | 21 | AAAB33310 | Pinus radiata tran |
| 36 | 449.5 | 36.2 | 242 | 19 | AAW48622  | Pinus radiata cone |
| 37 | 448.5 | 36.1 | 250 | 21 | AAO17679  | Plant flowering ti |
| 38 | 444   | 35.7 | 281 | 21 | AAAG29741 | Arabidopsis thalia |
| 39 | 443.5 | 35.7 | 205 | 23 | ABG60922  | Novel floral meris |
| 40 | 429   | 34.5 | 240 | 21 | AAAY96767 | Z. mays MADS-box p |
| 41 | 428.5 | 34.5 | 250 | 20 | AAW84048  | Rice OSMADS6 prote |
| 42 | 427   | 34.4 | 252 | 21 | AAAG29742 | Arabidopsis thalia |
| 43 | 425   | 34.2 | 270 | 22 | AAAB68357 | Amino acid sequenc |
| 44 | 424   | 34.1 | 228 | 23 | ABG60925  | Novel floral meris |
| 45 | 424   | 34.1 | 245 | 23 | ABG60944  | Novel floral meris |

#### ALIGNMENTS

##### RESULT 1

AAW81000  
ID AAW81000 standard; Protein; 246 AA.

XX AAW81000;

XX 10-MAY-1999 (first entry)

XX Arabidopsis AGL5 polypeptide.

XX AGL5-like gene; agamous-like 5 gene; seed dispersal; dehiscence; transgenic plant.

XX Arabidopsis thaliana.

XX WO9900502-Al.

XX 07-JAN-1999.

XX 25-JUN-1998; 98WO-US13208.

XX 28-APR-1998; 98US-0067800.

XX 27-JUN-1997; 97US-0051030.

XX (REGC ) UNIV CALIFORNIA.

XX Ferrandiz C, Yanofsky MF;

XX WPI; 1999-095747/08.

XX N-PSDB; AAV99858, AAV99860.

XX Use of agamous-like nucleic acids - useful for the production of transgenic seed plants in which dehiscence is modified resulting in

PT delayed seed dispersal

XX Disclosure; Page 91-92; 126pp; English.

PS This is the deduced amino acid sequence of an Arabidopsis

XX agamous-like 5 (AGL5) polypeptide that is involved in the

CC regulation of dehiscence. A cDNA clone encoding AGL5 is provided

CC in AAV99860, and a genomic clone in AAV99858. The invention provides a

CC transgenic seed plant, such as an agl1 and agl5 double mutant, that

CC is characterized by delayed seed dispersal due to suppression of

CC AGL1 (see AAW80999) and AGL5 expression. The invention also provides

CC dehiscence zone regulatory elements, derived from the AGL1 or AGL5

CC gene, that confer selective expression upon an operatively linked

CC nucleic acid molecule in the valve margin or dehiscence zone of a

CC seed plant. The transgenic seed plants include members of the

CC Brassicaceae, such as rapeseed, and members of the Fabaceae, such

CC as soybean, pea, lentil and bean. A plant expression vector

CC comprising a dehiscence zone-selective regulatory element, and a

CC kit for producing the transgenic seed plants are also provided.

XX Sequence 246 AA;

SQ

Query Match 100.0%; Score 1242; DB 20; Length 246;

Best Local Similarity 100.0%; Pred. No. 1.8e-113;

Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MEGGASNEVAESSKKIGRGKTEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVAL 60

QY 61 VIFSTRGRLYEVANNVRGTTIERYKKACSDAVNPPTITEANTQYQQEASKLRQIRDIQ 120

Db 61 VIFSTRGRLYEVANNVRGTTIERYKKACSDAVNPPTITEANTQYQQEASKLRQIRDIQ 120

QY 121 NLNRHILGESLGNLFKELKNLESRLKGISRVRSKKHEMLVAEIEYMQKREIELQNDNM 180

Db 121 NLNRHILGESLGNLFKELKNLESRLKGISRVRSKKHEMLVAEIEYMQKREIELQNDNM 180

QY 181 YLRSKITERTGLQQOESSVIHQGTVYESGVTSHQSGQYNNRYIAVNLLEPNQNSSNQDQ 240

Db 181 YLRSKITERTGLQQOESSVIHQGTVYESGVTSHQSGQYNNRYIAVNLLEPNQNSSNQDQ 240

QY 241 PPLQLV 246

Db 241 PPLQLV 246

RESULT 2

AAG32583

ID AAG32583 standard; Protein; 258 AA.

XX AAG32583;

AC

XX 17-OCT-2000 (first entry)

DT

XX Arabidopsis thaliana protein fragment SEQ ID NO: 39337.

DE

XX protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.

XX Arabidopsis thaliana.

OS

XX EP1033405-A2.

PN

XX 06-SEP-2000.

PD

XX 25-FEB-2000; 2000EP-0301439.

PF

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

\*PR

25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

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PR 30-APR-1999; 99US-0132048.

PR 05-MAY-1999; 99US-0132484.

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PR 30-JUN-1999; 99US-0141287.

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PR 12-JUL-1999; 99US-0142977.

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PR 28-OCT-1999; 99US-0161920.  
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QY 241 PPLQL 245  
Db 241 PPLQL 245

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AC AAW80999;  
XX  
DT 10-MAY-1999 (first entry)  
XX  
DE Arabidopsis AGL1 polypeptide.  
XX  
KW AGL1-like gene; agamous-like 1 gene; seed dispersal; dehiscence;  
KW transgenic plant.  
XX  
OS Arabidopsis thaliana.  
XX  
PN WO9900502-A1.  
XX





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| PR | 24-JUN-1999; | 99US-0140695; |
| PR | 28-JUN-1999; | 99US-0140823; |
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| PR | 21-JUL-1999; | 99US-0144814; |
| PR | 21-JUL-1999; | 99US-0145086; |
| PR | 21-JUL-1999; | 99US-0145087; |
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Query Match 84.5%; Score 1050; DB 21; Length 248;  
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|    |     |                                                              |     |
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| QY | 1   | MEGGASNEVAESSKIGRGKIEIKRIENTNRQVTFCKRRNGLLKKAYELSVLCDAEVAL   | 60  |
| Db | 1   | MEGGSSHDAESSKLGKIEIKRIENTNRQVTFCKRRNGLLKKAYELSVLCDAEVAL      | 60  |
| QY | 61  | VIFSTRGRLEYANNVSRGTIERYKKACSDAVNPPTITEANTYYQOEASKLRRTIDIQ    | 120 |
| Db | 61  | VIFSTRGRLEYANNVSRGTIERYKKACSDAVNPSPVTEANTYYQOEASKLRRTIDIQ    | 120 |
| QY | 121 | NLNRHILGESLGNFKELKNLESLEKGISRVRSKKHEMLVAEITYMQKREIELQNDNM    | 180 |
| Db | 121 | NSNRHIVGESLGNFKELKNLEGRLEKGISRVRSKKNELLVAEITYMQKREMELOHNNM   | 180 |
| QY | 181 | YLRSKITE--RTGLQQQESSVHQGTVYESGVTSSSHQSGQYNNRYIAVNLLLEPNQSSNQ | 238 |
| Db | 181 | YLRAKIAEGARLNPQQQESSVIOGTTVYESGVSSHDSQHYNNRYIPVNLLLEPNQOFSQ  | 240 |
| QY | 239 | DQPPLOLV                                                     | 246 |
| Db | 241 | DQPPLOLV                                                     | 248 |

## RESULT 5







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FH Key          Location/Qualifiers
FT Domain      16..72
FT             /note= "MADS domain"
FT Domain      106..172
FT             /note= "K-domain"
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XX CA2319853-A1.
XX
XX 01-APR-2001.
XX
XX 02-OCT-2000; 2000CA-2319853.
XX
XX 01-OCT-1999; 99US-0410464.
XX
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX
XX Rottman WH, Strauss SH, Brunner AM, Sheppard LA;
XX
XX WPI; 2001-336098/36.
XX
XX N-PSDB; AAF85400, AAF85401, AAF85402.
XX
XX Novel isolated polynucleotide derived from Populus species, useful for
XX producing transgenic plants having modified fertility characteristic,
XX particularly sterility -
XX
XX Claim 23; Page 62-63; 69pp; English.
XX
XX The present sequence represents a floral homeotic protein, designated
XX PTAG-2, which is derived from Populus balsamifera subsp. trichocarpa.
XX The specification also describes PTD, PTLF, and PTAG-1 proteins. The
XX floral homeotic proteins are expressed in floral tissues. PTLF is a
XX homologue of LEAFY (LFY) and FLORICAULA (FLO), and is expressed in
XX immature inflorescences on which floral primordia are developing. PTD
XX is a homologue of DEFICIENS (DEF), and is strongly expressed in stamen
XX primordia from the onset of organogenesis. PTAG-1 and PTAG-2 are
XX homologues of AGAMOUS (AG). The floral homeotic proteins and
XX polynucleotides are useful for producing transgenic plants having
XX modified fertility characteristics, particularly sterility.
XX
XX Sequence 238 AA;
XX
XX Query Match          57.9%; Score 719.5; DB 22; Length 238;
XX Best Local Similarity 62.3%; Pred. No. 3.1e-62;
XX Matches 147; Conservative 39; Mismatches 43; Indels 7; Gaps 3;
XX
QY 7 NEVAESS--KKTGRGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVALVIFS 64
Db ||| :|||:|||||:|||||:| :||| :|||:|||||:|||||:|||||:|||||:|||||:
5 NEPOESSPLRKLGRGKVEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVALVIFS 64
QY :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 65 SRGRLYEYNNSVKSTIERYKKACADSSNGSVSEANAQFYQOEAAKLRQIGNLQNSNR 124
QY 125 HILGESLGSNLFKELKNLESRLKGISRVRSKKHEMLVAEIEYMQKREIELQNDNMYLRS 184
Db :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
125 NMLGESLSALSVELKSLKLEKIGIRSKKNELLFAEIEYMQKREIDLHNNQLLRA 184
QY 185 KITERGLQOQESSVIHQTVYESGVTSSHQSGQYNNRYIAVNLLEPNQNSNQDQ 240
Db ||| :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
185 KIAENE-RKRQHMLMPGGVNFIMQSPFDS---RNYSQVNGLPANHYHPEDQ 235

RESULT 11
ABG30868
ID ABG30868 standard; Protein; 238 AA.
XX
XX ABG30868;
XX
XX 07-OCT-2002 (first entry)
XX
XX Poplar floral homeotic protein PTAG-2.
XX
XX Poplar; plant; DEFICIENS; transgenic; promoter;
KW protein transduction domain; floral homeotic gene;
KW floral-specific expression; cytotoxin; fertility; sterility;
KW PTLF; PTAG-1; PTAG-2.
XX
XX Populus balsamifera subsp. trichocarpa.
XX
XX Key          Location/Qualifiers
XX FH Domain    16..72
XX FT           /label= MADS_domain
XX FT           /note= "MADS is named for the first 4 proteins in
XX FT           which it was discovered, yeast minichromosome maintenance
XX FT           factor, floral homeotic genes AG and DEF and human serum
XX FT           response factor"
XX FT           106..172
XX FT           /label= K_domain
XX
XX US6395892-B1.
XX
XX 28-MAY-2002.
XX
XX 01-OCT-1999; 99US-0410464.
XX
XX 06-APR-1998; 98US-080851p.
XX
XX 06-APR-1999; 99US-0287700.
XX
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX
XX Strauss SH, Rottmann W, Brunner A, Sheppard L;
XX
XX WPI; 2002-572853/61.
XX
XX N-PSDB; ABR88490, ABR88491.
XX
XX New protein transduction domain promoter nucleic acid molecule useful
XX for producing transgenic plants having modified fertility
XX characteristics, particularly sterility -
XX
XX Disclosure; Column 81-84; 46pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule especially a
XX protein transduction domain (PTD) promoter: (i) that hybridises under
XX wash conditions of 0.2 x SSC (saline sodium citrate), 0.1 %SDS (sodium
XX dodecyl sulphate) at 65 plusOC to nucleotides or (ii) comprising 35
XX consecutive nucleotides of the PTD gene. PTD is a floral homeotic
XX gene and is the homologue of DEFICIENS. Also includes are a recombinant
XX nucleic acid comprising the PTD promoter, a cell transformed with
XX the recombinant nucleic acid and a transgenic plant comprising the
XX transformed cell. The PTD promoter is useful to obtain floral-specific
XX expression of genes such as cytotoxins, that are employed in genetic
XX ablation strategies to produce trees having modified fertility
XX characteristics, including sterility. Genetic constructs comprising
XX antisense versions or dominant negative mutants of PTD are useful in
XX producing genetically engineered Poplars and other trees, and for sense
XX suppression. Also disclosed are 3 other homeotic genes PTLF, PTAG-1
XX and PTAG-2 (none are defined). The present sequence is the PTAG-2
XX protein.
XX
XX Sequence 238 AA;
XX
XX Query Match          57.9%; Score 719.5; DB 23; Length 238;
XX Best Local Similarity 62.3%; Pred. No. 3.1e-62;
XX Matches 147; Conservative 39; Mismatches 43; Indels 7; Gaps 3;
XX
QY 7 NEVAESS--KKTGRGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVALVIFS 64
Db ||| :|||:|||||:|||||:| :||| :|||:|||||:|||||:|||||:|||||:|||||:
5 NEPOESSPLRKLGRGKVEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVALVIFS 64
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Db 65 SRGRLYEYNNSVKSTIERYKKACADSSNGSVSEANAQFYQOEAAKLRQIGNLQNSNR 124
QY 125 HILGESLGSNLFKELKNLESRLKGISRVRSKKHEMLVAEIEYMQKREIELQNDNMYLRS 184
Db :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
125 NMLGESLSALSVELKSLKLEKIGIRSKKNELLFAEIEYMQKREIDLHNNQLLRA 184
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 DT 17-OCT-2000 (first entry)  
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 KW termination sequence.  
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 OS Arabidopsis thaliana.  
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PR 05-AUG-1999; 99US-0147192.

PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159638.  
PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160768.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match

56.9%; Score 706.5; DB 21; Length 277;

|                                                                                                                   |                                                                          |                                                               |     |  |  |  |  |  |  |
|-------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------|---------------------------------------------------------------|-----|--|--|--|--|--|--|
| Best Local Similarity 61.9%; Pred. No. 7.3e-61;<br>Matches 138; Conservative 34; Mismatches 44; Indels 7; Gaps 1; |                                                                          |                                                               |     |  |  |  |  |  |  |
| QY                                                                                                                | 15                                                                       | KIGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGRLEYAN   | 74  |  |  |  |  |  |  |
| Db                                                                                                                | 47                                                                       | RMGRGKIEIKRIENSTNRQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGRLEYAN   | 106 |  |  |  |  |  |  |
| QY                                                                                                                | 75                                                                       | NSVRGTIERKKACSDAVNPPTITEANTQYYQOEAASKLRQIRDIONLRHILGESLGS     | 134 |  |  |  |  |  |  |
| Db                                                                                                                | 107                                                                      | NNIRSTIERKKACSDSTNTSTVQEIENAAYYQOESAKLRQIQIQTIONSNRNLMGDSLSSL | 166 |  |  |  |  |  |  |
| QY                                                                                                                | 135                                                                      | NFKELKNLESRLKGIISRVRSKKHEMLVAEIEYMQKEIEIQNDNMVLSKITERTGLQ     | 194 |  |  |  |  |  |  |
| Db                                                                                                                | 167                                                                      | SVKELQOVENRLEKAISRIRSKHELLVLEIENAAQKREIELDNENIYLRTKVAEVERYQQ  | 226 |  |  |  |  |  |  |
| QY                                                                                                                | 195                                                                      | QESSVHOGTVYESGVTSSHQSGQYNNRYIAVNLLEPNQNSSN                    | 237 |  |  |  |  |  |  |
| Db                                                                                                                | 227                                                                      | HHQMV-----SGSEINAIEALASRNYFAHSIMTAGSGSGN                      | 262 |  |  |  |  |  |  |
| RESULT 14                                                                                                         |                                                                          |                                                               |     |  |  |  |  |  |  |
| ID                                                                                                                | AAG40212                                                                 |                                                               |     |  |  |  |  |  |  |
| XX                                                                                                                | AAG40212 standard; Protein; 277 AA.                                      |                                                               |     |  |  |  |  |  |  |
| AC                                                                                                                | AAG40212;                                                                |                                                               |     |  |  |  |  |  |  |
| DT                                                                                                                | 18-OCT-2000 (first entry)                                                |                                                               |     |  |  |  |  |  |  |
| DE                                                                                                                | Arabidopsis thaliana protein fragment SEQ ID NO: 49864.                  |                                                               |     |  |  |  |  |  |  |
| XX                                                                                                                | Protein identification; signal transduction pathway; metabolic pathway;  |                                                               |     |  |  |  |  |  |  |
| KW                                                                                                                | hybridisation assay; genetic mapping; gene expression control; promoter; |                                                               |     |  |  |  |  |  |  |
| KW                                                                                                                | termination sequence.                                                    |                                                               |     |  |  |  |  |  |  |
| XX                                                                                                                | Arabidopsis thaliana.                                                    |                                                               |     |  |  |  |  |  |  |
| OS                                                                                                                | EP1033405-A2.                                                            |                                                               |     |  |  |  |  |  |  |
| XX                                                                                                                | 06-SEP-2000.                                                             |                                                               |     |  |  |  |  |  |  |
| XX                                                                                                                | 25-FEB-2000; 2000EP-0301439.                                             |                                                               |     |  |  |  |  |  |  |
| PR                                                                                                                | 25-FEB-1999; 99US-0121825.                                               |                                                               |     |  |  |  |  |  |  |
| PR                                                                                                                | 05-MAR-1999; 99US-0123180.                                               |                                                               |     |  |  |  |  |  |  |
| PR                                                                                                                | 09-MAR-1999; 99US-0123548.                                               |                                                               |     |  |  |  |  |  |  |
| PR                                                                                                                | 23-MAR-1999; 99US-0125788.                                               |                                                               |     |  |  |  |  |  |  |
| PR                                                                                                                | 25-MAR-1999; 99US-0126264.                                               |                                                               |     |  |  |  |  |  |  |
| PR                                                                                                                | 29-MAR-1999; 99US-0126785.                                               |                                                               |     |  |  |  |  |  |  |
| PR                                                                                                                | 01-APR-1999; 99US-0127462.                                               |                                                               |     |  |  |  |  |  |  |
| PR                                                                                                                | 06-APR-1999; 99US-0128234.                                               |                                                               |     |  |  |  |  |  |  |
| PR                                                                                                                | 08-APR-1999; 99US-0128714.                                               |                                                               |     |  |  |  |  |  |  |
| PR                                                                                                                | 16-APR-1999; 99US-0129845.                                               |                                                               |     |  |  |  |  |  |  |
| PR                                                                                                                | 19-APR-1999; 99US-0130077.                                               |                                                               |     |  |  |  |  |  |  |
| PR                                                                                                                | 21-APR-1999; 99US-0130449.                                               |                                                               |     |  |  |  |  |  |  |
| PR                                                                                                                | 23-APR-1999; 99US-0130510.                                               |                                                               |     |  |  |  |  |  |  |
| PR                                                                                                                | 23-APR-1999; 99US-0130891.                                               |                                                               |     |  |  |  |  |  |  |
| PR                                                                                                                | 28-APR-1999; 99US-0131449.                                               |                                                               |     |  |  |  |  |  |  |
| PR                                                                                                                | 30-APR-1999; 99US-0132048.                                               |                                                               |     |  |  |  |  |  |  |
| PR                                                                                                                | 30-APR-1999; 99US-0132407.                                               |                                                               |     |  |  |  |  |  |  |
| PR                                                                                                                | 04-MAY-1999; 99US-0132484.                                               |                                                               |     |  |  |  |  |  |  |
| PR                                                                                                                | 05-MAY-1999; 99US-0132485.                                               |                                                               |     |  |  |  |  |  |  |
| PR                                                                                                                | 06-MAY-1999; 99US-0132486.                                               |                                                               |     |  |  |  |  |  |  |
| PR                                                                                                                | 06-MAY-1999; 99US-0132487.                                               |                                                               |     |  |  |  |  |  |  |
| PR                                                                                                                | 07-MAY-1999; 99US-0132863.                                               |                                                               |     |  |  |  |  |  |  |
| PR                                                                                                                | 11-MAY-1999; 99US-0134256.                                               |                                                               |     |  |  |  |  |  |  |
| PR                                                                                                                | 14-MAY-1999; 99US-0134218.                                               |                                                               |     |  |  |  |  |  |  |
| PR                                                                                                                | 14-MAY-1999; 99US-0134219.                                               |                                                               |     |  |  |  |  |  |  |
| PR                                                                                                                | 14-MAY-1999; 99US-0134221.                                               |                                                               |     |  |  |  |  |  |  |
| PR                                                                                                                | 14-MAY-1999; 99US-0134370.                                               |                                                               |     |  |  |  |  |  |  |
| PR                                                                                                                | 18-MAY-1999; 99US-0134768.                                               |                                                               |     |  |  |  |  |  |  |
| PR                                                                                                                | 19-MAY-1999; 99US-0134941.                                               |                                                               |     |  |  |  |  |  |  |
| PR                                                                                                                | 20-MAY-1999; 99US-0135124.                                               |                                                               |     |  |  |  |  |  |  |
| PR                                                                                                                | 21-MAY-1999; 99US-0135353.                                               |                                                               |     |  |  |  |  |  |  |

|                                                                |                                                                          |                                                                  |
|----------------------------------------------------------------|--------------------------------------------------------------------------|------------------------------------------------------------------|
| PR                                                             | 02-AUG-1999;                                                             | 99US-0146389.                                                    |
| PR                                                             | 03-AUG-1999;                                                             | 99US-0147038.                                                    |
| PR                                                             | 04-AUG-1999;                                                             | 99US-0147204.                                                    |
| PR                                                             | 04-AUG-1999;                                                             | 99US-0147302.                                                    |
| PR                                                             | 05-AUG-1999;                                                             | 99US-0147192.                                                    |
| PR                                                             | 05-AUG-1999;                                                             | 99US-0147260.                                                    |
| PR                                                             | 06-AUG-1999;                                                             | 99US-0147303.                                                    |
| PR                                                             | 06-AUG-1999;                                                             | 99US-0147416.                                                    |
| PR                                                             | 09-AUG-1999;                                                             | 99US-0147493.                                                    |
| PR                                                             | 09-AUG-1999;                                                             | 99US-0147935.                                                    |
| PR                                                             | 10-AUG-1999;                                                             | 99US-0148171.                                                    |
| PR                                                             | 11-AUG-1999;                                                             | 99US-0148319.                                                    |
| PR                                                             | 12-AUG-1999;                                                             | 99US-0148341.                                                    |
| PR                                                             | 13-AUG-1999;                                                             | 99US-0148565.                                                    |
| PR                                                             | 13-AUG-1999;                                                             | 99US-0148684.                                                    |
| PR                                                             | 16-AUG-1999;                                                             | 99US-0149368.                                                    |
| PR                                                             | 17-AUG-1999;                                                             | 99US-0149175.                                                    |
| PR                                                             | 18-AUG-1999;                                                             | 99US-0149426.                                                    |
| PR                                                             | 20-AUG-1999;                                                             | 99US-0149722.                                                    |
| PR                                                             | 20-AUG-1999;                                                             | 99US-0149723.                                                    |
| PR                                                             | 20-AUG-1999;                                                             | 99US-0149929.                                                    |
| PR                                                             | 23-AUG-1999;                                                             | 99US-0149902.                                                    |
| PR                                                             | 23-AUG-1999;                                                             | 99US-0149930.                                                    |
| PR                                                             | 25-AUG-1999;                                                             | 99US-0150366.                                                    |
| PR                                                             | 26-AUG-1999;                                                             | 99US-0150884.                                                    |
| PR                                                             | 27-AUG-1999;                                                             | 99US-0151065.                                                    |
| PR                                                             | 27-AUG-1999;                                                             | 99US-0151066.                                                    |
| PR                                                             | 27-AUG-1999;                                                             | 99US-0151080.                                                    |
| PR                                                             | 30-AUG-1999;                                                             | 99US-0151303.                                                    |
| PR                                                             | 31-AUG-1999;                                                             | 99US-0151438.                                                    |
| PR                                                             | 01-SEP-1999;                                                             | 99US-0151930.                                                    |
| PR                                                             | 07-SEP-1999;                                                             | 99US-0152363.                                                    |
| PR                                                             | 10-SEP-1999;                                                             | 99US-0153070.                                                    |
| PR                                                             | 13-SEP-1999;                                                             | 99US-0153758.                                                    |
| PR                                                             | 15-SEP-1999;                                                             | 99US-0154018.                                                    |
| PR                                                             | 16-SEP-1999;                                                             | 99US-0154039.                                                    |
| PR                                                             | 20-SEP-1999;                                                             | 99US-0154779.                                                    |
| PR                                                             | 23-SEP-1999;                                                             | 99US-0155139.                                                    |
| PR                                                             | 23-SEP-1999;                                                             | 99US-0155486.                                                    |
| PR                                                             | 24-SEP-1999;                                                             | 99US-0155659.                                                    |
| PR                                                             | 28-SEP-1999;                                                             | 99US-0156458.                                                    |
| PR                                                             | 29-SEP-1999;                                                             | 99US-0156596.                                                    |
| PR                                                             | 04-OCT-1999;                                                             | 99US-0157117.                                                    |
| PR                                                             | 05-OCT-1999;                                                             | 99US-0157753.                                                    |
| PR                                                             | 06-OCT-1999;                                                             | 99US-0157865.                                                    |
| PR                                                             | 07-OCT-1999;                                                             | 99US-0158029.                                                    |
| PR                                                             | 08-OCT-1999;                                                             | 99US-0158232.                                                    |
| PR                                                             | 12-OCT-1999;                                                             | 99US-0158369.                                                    |
| PR                                                             | 13-OCT-1999;                                                             | 99US-0159293.                                                    |
| PR                                                             | 13-OCT-1999;                                                             | 99US-0159294.                                                    |
| PR                                                             | 13-OCT-1999;                                                             | 99US-0159295.                                                    |
| PR                                                             | 14-OCT-1999;                                                             | 99US-0159329.                                                    |
| PR                                                             | 14-OCT-1999;                                                             | 99US-0159330.                                                    |
| PR                                                             | 14-OCT-1999;                                                             | 99US-0159331.                                                    |
| PR                                                             | 14-OCT-1999;                                                             | 99US-0159637.                                                    |
| PR                                                             | 14-OCT-1999;                                                             | 99US-0159638.                                                    |
| PR                                                             | 18-OCT-1999;                                                             | 99US-0159584.                                                    |
| PR                                                             | 21-OCT-1999;                                                             | 99US-0160741.                                                    |
| PR                                                             | 21-OCT-1999;                                                             | 99US-0160767.                                                    |
| PR                                                             | 21-OCT-1999;                                                             | 99US-0160768.                                                    |
| PR                                                             | 21-OCT-1999;                                                             | 99US-0160770.                                                    |
| PR                                                             | 21-OCT-1999;                                                             | 99US-0160814.                                                    |
| PR                                                             | 21-OCT-1999;                                                             | 99US-0160815.                                                    |
| PR                                                             | 22-OCT-1999;                                                             | 99US-0160980.                                                    |
| PR                                                             | 22-OCT-1999;                                                             | 99US-0160981.                                                    |
| PR                                                             | 22-OCT-1999;                                                             | 99US-0160989.                                                    |
| PR                                                             | 25-OCT-1999;                                                             | 99US-0161404.                                                    |
| PR                                                             | 25-OCT-1999;                                                             | 99US-0161405.                                                    |
| PR                                                             | 25-OCT-1999;                                                             | 99US-0161406.                                                    |
| PR                                                             | 26-OCT-1999;                                                             | 99US-0161359.                                                    |
| PR                                                             | 26-OCT-1999;                                                             | 99US-0161360.                                                    |
| PR                                                             | 26-OCT-1999;                                                             | 99US-0161361.                                                    |
| PR                                                             | 28-OCT-1999;                                                             | 99US-0161920.                                                    |
| PR                                                             | 02-AUG-1999;                                                             | 99US-0161992.                                                    |
| PR                                                             | 28-OCT-1999;                                                             | 99US-0161993.                                                    |
| PR                                                             | 29-OCT-1999;                                                             | 99US-0162142.                                                    |
| Query Match 56.9%; Score 706.5; DB 21; Length 277;             |                                                                          |                                                                  |
| Best Local Similarity 61.9%; Pred. No. 7.3e-61;                |                                                                          |                                                                  |
| Matches 138; Conservative 34; Mismatches 44; Indels 7; Gaps 1; |                                                                          |                                                                  |
| QY                                                             | 15                                                                       | KIGRGKIEIKRIENTNRQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGRLEYAN 74    |
| Db                                                             | 47                                                                       | RMGRGKIEIKRIENSTNRQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGRLEYAN 106  |
| QY                                                             | 75                                                                       | NSVRGTIERKKACSDAVNPPTITEANTQYYQEQEASKLRQIRDIONLRHILGESLGL 134    |
| Db                                                             | 107                                                                      | NNIRSTIERKKACSDSTNTSTVQEIINAAYYQEQESAKLRQIQTIQNSNRNLMGDSLSSL 166 |
| QY                                                             | 135                                                                      | NFKELKNLESRLKGISRVRSKKHEMLVAEIEYMQKRIELQNDNMYLRSKITERTGLQO 194   |
| Db                                                             | 167                                                                      | SVKELQOVENRLEKAISRIRSKHELLLVEIENAKQRIELDNEINIYLRTKVAEVERYQO 226  |
| QY                                                             | 195                                                                      | QESSVIHQGVYESGVTSSHQSGQYRNRYIAVNLLPEQNQSSN 237                   |
| Db                                                             | 227                                                                      | HHQMV-----SGSEINAIEALASRNIFYAHSINTAGSGGN 262                     |
| RESULT 15                                                      |                                                                          |                                                                  |
| AAG16690                                                       |                                                                          |                                                                  |
| ID                                                             | AAG16690 standard; Protein; 230 AA.                                      |                                                                  |
| XX                                                             | AAG16690;                                                                |                                                                  |
| AC                                                             | AAG16690;                                                                |                                                                  |
| XX                                                             | 17-OCT-2000 (first entry)                                                |                                                                  |
| DT                                                             | Arabidopsis thaliana protein fragment SEQ ID NO: 17433.                  |                                                                  |
| DE                                                             | Protein identification; signal transduction pathway; metabolic pathway;  |                                                                  |
| XX                                                             | hybridisation assay; genetic mapping; gene expression control; promoter; |                                                                  |
| KW                                                             | termination sequence.                                                    |                                                                  |
| KW                                                             | Arabidopsis thaliana.                                                    |                                                                  |
| XX                                                             | EP1033405-A2.                                                            |                                                                  |
| XX                                                             | 06-SEP-2000.                                                             |                                                                  |
| XX                                                             | 25-FEB-2000; 2000EP-0301439.                                             |                                                                  |
| PF                                                             | 99US-0121825.                                                            |                                                                  |
| XX                                                             | 99US-0123180.                                                            |                                                                  |
| PR                                                             | 99US-0123548.                                                            |                                                                  |
| PR                                                             | 99US-0125788.                                                            |                                                                  |
| PR                                                             | 99US-0126264.                                                            |                                                                  |
| PR                                                             | 99US-0126785.                                                            |                                                                  |
| PR                                                             | 99US-0127462.                                                            |                                                                  |
| PR                                                             | 99US-0128234.                                                            |                                                                  |
| PR                                                             | 99US-0128714.                                                            |                                                                  |
| PR                                                             | 99US-0129845.                                                            |                                                                  |
| PR                                                             | 99US-0130077.                                                            |                                                                  |
| PR                                                             | 99US-0130449.                                                            |                                                                  |
| PR                                                             | 99US-0130510.                                                            |                                                                  |
| PR                                                             | 99US-0130891.                                                            |                                                                  |
| PR                                                             | 99US-0131449.                                                            |                                                                  |
| PR                                                             | 99US-0132048.                                                            |                                                                  |
| PR                                                             | 99US-0132407.                                                            |                                                                  |
| PR                                                             | 99US-0132484.                                                            |                                                                  |
| PR                                                             | 99US-0132485.                                                            |                                                                  |
| PR                                                             | 99US-0132486.                                                            |                                                                  |
| PR                                                             | 99US-0132487.                                                            |                                                                  |
| PR                                                             | 99US-0132863.                                                            |                                                                  |
| PR                                                             | 99US-0134256.                                                            |                                                                  |
| PR                                                             | 99US-0134218.                                                            |                                                                  |
| PR                                                             | 99US-0134219.                                                            |                                                                  |
| PR                                                             | 99US-0134221.                                                            |                                                                  |

PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
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PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
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PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
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PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
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PR 24-JUN-1999; 99US-0140695.  
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Job time : 31.3725 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 27, 2003, 12:43:08 ; Search time 13.4453 Seconds  
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Title: US-09-978-382A-6  
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Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1  
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; Sequence 8, Application US/09067800  
; Patent No. 6198024  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin F.  
; APPLICANT: Ferrandiz, Cristina  
; TITLE OF INVENTION: Seed Plants Characterized by Delayed  
; TITLE OF INVENTION: Seed Dispersal  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/067,800  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UD 2948  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 246 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-067-800-8

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RESULT 2  
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; Patent No. 6288305  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin F.  
; APPLICANT: Ferrandiz, Cristina  
; TITLE OF INVENTION: Seed Plants Characterized by Delayed  
; TITLE OF INVENTION: Seed Dispersal  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/349,677  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/067,800  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UD 2948  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 246 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-349-677-8

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US-09-067-800-6  
; Sequence 6, Application US/09067800  
; Patent No. 6198024  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin F.  
; APPLICANT: Ferrandiz, Cristina  
; TITLE OF INVENTION: Seed Plants Characterized by Delayed  
; TITLE OF INVENTION: Seed Dispersal  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/067,800  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UD 2948  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 248 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-067-800-6

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## RESULT 4

US-09-349-677-6  
; Sequence 6, Application US/09349677  
; Patent No. 6288305  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin F.  
; APPLICANT: Ferrandiz, Cristina  
; TITLE OF INVENTION: Seed Plants Characterized by Delayed  
; TITLE OF INVENTION: Seed Dispersal  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/349,677  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/067,800  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UD 2948  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 248 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-349-677-6

Query Match 84.5%; Score 1050; DB 4; Length 248;  
Best Local Similarity 85.5%; Pred. No. 3.5e-98;  
Matches 212; Conservative 12; Mismatches 22; Indels 2; Gaps 1;  
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QY 121 NLNRHILGESLGNFKELKNLESRLKGISRVRSKKHEMLVAEIEYMKREIELQNDNM 180  
Db 121 NSNRHIVGESLGNFKELKNLEGRLEKGISRVRSKKNELVAEIEYMKREMELOHNMM 180  
QY 181 YLRSKITE--RTGLQOQESSVIHQGTIVYESGVTSSHQSGQYNNRYTAVNLEPNQSSNQ 238  
Db 181 YLRKIAEGARLNPDOQESSVIQGTIVYESGVSSHDSQSHYNNRYIPVNLLEPNQOFSQ 240  
QY 239 DQPPQLV 246  
Db 241 DQPPQLV 248

## RESULT 5

US-08-460-512-7  
; Sequence 7, Application US/08460512  
; Patent No. 5744693  
; GENERAL INFORMATION:  
; APPLICANT: MEYEROWITZ, Elliot M.  
; APPLICANT: YANOFISKY, Martin F.  
; APPLICANT: MA, Hong  
; TITLE OF INVENTION: PLANTS HAVING ALTERED FLORAL DEVELOPMENT  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Richard F. Trecartin  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/460,512  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/293,278  
; FILING DATE:  
; APPLICATION NUMBER: US/07/956,694  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Trecartin, Richard F.  
; REGISTRATION NUMBER: 31,801  
; REFERENCE/DOCKET NUMBER: A-57322/RFT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 248 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-460-512-7

Query Match 62.8%; Score 780.5; DB 1; Length 248;  
Best Local Similarity 66.9%; Pred. No. 5.9e-71;  
Matches 158; Conservative 34; Mismatches 39; Indels 5; Gaps 3;  
QY 14 KKIGRGKIEIKRIENTTNRQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLEYA 73  
Db 15 KKLGRGKIEIKRIENTTNRQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLEYA 74  
QY 74 NNSVGTIERYKACSDAVNPPTITEANTQYYQOEASKLRRQIRDIQNLRHILGESLGS 133  
Db 75 NNSVKATIERYKACSDSSNTGTSSEANQYYQOEASKLRAQIGNLQNRNMLGESLAA 134  
QY 134 LNFELKNLESRLKGISRVRSKKHEMLVAEIEYMKRETELQNDNMVLRSKI--TERTG 191  
Db 135 LSLRDLKNLEQKIEKGISKIRSKNELFAEIEYMKREIDLHNNQYLRAKIAETERAQ 194  
QY 192 LQQOQESSV-IHQGTIVYESGVTSSHQSGQYNNRYTAVNLEPNQSSNQDQPPQLV 246  
Db 195 QQQQQQQMNLMPGSSSYELVPPPHQFD--TRNYLQVNGLTNNHVTRODQPSQLV 248  
RESULT 6  
US-09-433-579-2  
; Sequence 2, Application US/09433579  
; Patent No. 6444877  
; GENERAL INFORMATION:

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; APPLICANT: Rottmann, William H.
; TITLE OF INVENTION: LSAG Gene
; FILE REFERENCE: LSAG Gene
; CURRENT APPLICATION NUMBER: US/09/433,579
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Liquidambar styraciflua
US-09-433-579-2

Query Match 61.6%; Score 764.5; DB 4; Length 226;
Best Local Similarity 67.5%; Pred. No. 2.1e-69;
Matches 156; Conservative 30; Mismatches 40; Indels 5; Gaps 2;

Qy 16 IGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGRLYEYANN 75
Db 1 MGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGRLYEYANN 60

Qy 76 SVRGTTIYKACSDAVNPPTITEANTQYQOEASKLRQIRDIONLNRHILGESLSLN 135
Db 61 SVKATTIYKASVDSNTGVSSEANAQFYQOEAGKLRNQNMTNRTMLGESLSLS 120

Qy 136 FKELKLESLNFKELKNLESRLKGISRVRSKKHMLVAEIEYMKREIELQNDNMVLRSKITERTGLQOQ 195
Db 121 PKELKLETKLEKGISKIRSKNELLFSEIEYMKREIELDHNQYLRAKIAEHERAQOQ 180

Qy 196 ESSVIHOGTVYESGVTSSHQSGQYNNRYIAVNLLEPNQSSNQDQPLQLV 246
Db 181 -MNLMPGGSNYEVLPSQFDS----RNFFQVNALQPNHHYSRQDQMALQLV 226

RESULT 7
US-09-410-464-12
; Sequence 12, Application US/09410464
; Patent No. 6395892
; GENERAL INFORMATION:
; APPLICANT: Strauss et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; FILE REFERENCE: 53375
; CURRENT APPLICATION NUMBER: US/09/410,464
; CURRENT FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: 09/287,700
; EARLIER FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,851
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Populus balsamifera subsp. trichocarpa
US-09-410-464-12

Query Match 60.1%; Score 746.5; DB 4; Length 241;
Best Local Similarity 63.2%; Pred. No. 1.5e-67;
Matches 153; Conservative 41; Mismatches 41; Indels 7; Gaps 3;

Qy 7 NEVAESS--KKIGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALVIFS 64
Db 5 NESLESSPLRKLGKRGKVEIKRIENTTNQVTFCKRRSGLLKKAYELSVLCDAEVALVIFS 64

Qy 65 TRGRLYEYANNVSRGTIYKACSDAVNPPTITEANTQYQOEASKLRQIRDIONLNR 124
Db 65 SRGRLYEYSDSVKSTIYKACSDSSNNGSVSEANAQFYQOEAKLRQIGNLQNSNR 124

Qy 125 HILGESLSLNFELKNLESRLKGISRVRSKKHMLVAEIEYMKREIELQNDNMVLR 184
Db 125 HMLGEALSSLSVKELKSLKLEKIGIRSKIRSKNELLFAEIEYMKREIVOLHNNQLLRA 184

Query Match 61.6%; Score 764.5; DB 4; Length 226;
Best Local Similarity 67.5%; Pred. No. 2.1e-69;
Matches 156; Conservative 30; Mismatches 40; Indels 5; Gaps 2;

Qy 16 IGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGRLYEYANN 75
Db 1 MGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGRLYEYANN 60

Qy 76 SVRGTTIYKACSDAVNPPTITEANTQYQOEASKLRQIRDIONLNRHILGESLSLN 135
Db 61 SVKATTIYKASVDSNTGVSSEANAQFYQOEAGKLRNQNMTNRTMLGESLSLS 120

Qy 136 FKELKLESLNFKELKNLESRLKGISRVRSKKHMLVAEIEYMKREIELQNDNMVLRSKITERTGLQOQ 195
Db 121 PKELKLETKLEKGISKIRSKNELLFSEIEYMKREIELDHNQYLRAKIAEHERAQOQ 180

Qy 196 ESSVIHOGTVYESGVTSSHQSGQYNNRYIAVNLLEPNQSSNQDQPLQLV 246
Db 181 -MNLMPGGSNYEVLPSQFDS----RNFFQVNALQPNHHYSRQDQMALQLV 226

RESULT 7
US-09-410-464-12
; Sequence 12, Application US/09410464
; Patent No. 6395892
; GENERAL INFORMATION:
; APPLICANT: Strauss et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; FILE REFERENCE: 53375
; CURRENT APPLICATION NUMBER: US/09/410,464
; CURRENT FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: 09/287,700
; EARLIER FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,851
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Populus balsamifera subsp. trichocarpa
US-09-410-464-12

Query Match 60.1%; Score 746.5; DB 4; Length 241;
Best Local Similarity 63.2%; Pred. No. 1.5e-67;
Matches 153; Conservative 41; Mismatches 41; Indels 7; Gaps 3;

Qy 7 NEVAESS--KKIGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALVIFS 64
Db 5 NESLESSPLRKLGKRGKVEIKRIENTTNQVTFCKRRSGLLKKAYELSVLCDAEVALVIFS 64

Qy 65 TRGRLYEYANNVSRGTIYKACSDAVNPPTITEANTQYQOEASKLRQIRDIONLNR 124
Db 65 SRGRLYEYSDSVKSTIYKACSDSSNNGSVSEANAQFYQOEAKLRQIGNLQNSNR 124

Qy 125 HILGESLSLNFELKNLESRLKGISRVRSKKHMLVAEIEYMKREIELQNDNMVLR 184
Db 125 HMLGEALSSLSVKELKSLKLEKIGIRSKIRSKNELLFAEIEYMKREIVOLHNNQLLRA 184
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Qy 185 KITERTGLQOQESSVIHQGTVYESGVTSSHQSGQYNNRYIAVNLLEPNQSSNQDQPLQ 244
Db 185 KISENE--RKRQSMNLMPGADFEIVQSQPYDS----RNYSQVNGLPASHYSHQDQMALQ 239

Qy 245 LV 246
Db 240 LV 241

RESULT 8
US-09-410-464-16
; Sequence 16, Application US/09410464
; Patent No. 6395892
; GENERAL INFORMATION:
; APPLICANT: Strauss et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; FILE REFERENCE: 53375
; CURRENT APPLICATION NUMBER: US/09/410,464
; CURRENT FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: 09/287,700
; EARLIER FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,851
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Populus balsamifera subsp. trichocarpa
US-09-410-464-16

Query Match 57.9%; Score 719.5; DB 4; Length 238;
Best Local Similarity 62.3%; Pred. No. 8e-65;
Matches 147; Conservative 39; Mismatches 43; Indels 7; Gaps 3;

Qy 7 NEVAESS--KKIGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALVIFS 64
Db 5 NEQESSPLRKLGKRGKVEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALVIFS 64

Qy 65 TRGRLYEYANNVSRGTIYKACSDAVNPPTITEANTQYQOEASKLRQIRDIONLNR 124
Db 65 SRGRLYEYSDSVKSTIYKACSDSSNNGSVSEANAQFYQOEAKLRQIGNLQNSNR 124

Qy 125 HILGESLSLNFELKNLESRLKGISRVRSKKHMLVAEIEYMKREIELQNDNMVLR 184
Db 125 NMLGESLSALSVKELKSLKLEKIGIRSKIRSKNELLFAEIEYMKREIDLHNNQLLRA 184

Qy 185 KITERTGLQOQESSVIHQGTVYESGVTSSHQSGQYNNRYIAVNLLEPNQSSNQDQ 240
Db 185 KIAENE--RKRQHMNLMPPGGVNFEMQSQPDS----RNYSQVNGLPANHYPHEDQ 235

RESULT 9
US-08-460-512-5
; Sequence 5, Application US/08460512
; Patent No. 5744693
; GENERAL INFORMATION:
; APPLICANT: MEYEROWITZ, Elliot M.
; APPLICANT: YANOFOSKY, Martin F.
; APPLICANT: MA, Hong
; TITLE OF INVENTION: PLANTS HAVING ALTERED FLORAL DEVELOPMENT
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard F. Trecartin
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; APPLICATION NUMBER: US/08/460,512
; FILING DATE: June 2, 1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,278
; FILING DATE: October 14, 1994
; APPLICATION NUMBER: US/07/956,694
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-57322/RFT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 252 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-460-512-4

Query Match 57.2%; Score 710.5; DB 1; Length 252;
Best Local Similarity 58.4%; Pred. No. 7.1e-64;
Matches 146; Conservative 39; Mismatches 54; Indels 11; Gaps 4;

QY 3 GCASNEVAESSKIGKGIETKRIENTNRQVTFCKRRNGLLKKAYELSVLCDAEVALVI 62
Db 8 GGESS-----PORKAGRGKIEIKRIENTNRQVTFCKRRNGLLKKAYELSVLCDAEVALVI 63
QY 63 FSTRGRLYEYANNVSRGTIERKKACSDAVNPPTITEANTQYQQEASKLRQIRDIONL 122
Db 64 FSSRGRLYEYNSNVKGTIERKKALSDNSNTGTVAEINAGYQQESAKLRQIIISQNS 123
QY 123 NRHILGSLGSLNFELKLNLSRLERKIGISRVRSKKHEMLVAEIEYMQKREIELQNDNMYL 182
Db 124 NQLMGFTIGSPKELNLEGRDLSVNRIRSKNELLFAIDYMQKREVDLHNDNQLL 183
QY 183 RSKITERTGLQQQESSVIHQGVYESGVTSSHQSGQ--YNRNYIAVNLLEPN---QNSS 236
Db 184 RAKIAENE-RNPNMSLMPGGSNYEIMPPPTQPPQDFDSRNYFQVAALQPNHHYSSAG 242
QY 237 NODOPPLQLV 246
Db 243 REDQATALQLV 252

RESULT 12
US-08-867-087B-13
; Sequence 13, Application US/08867087B
; Patent No. 5990386
; GENERAL INFORMATION:
; APPLICANT: An, Gynheung
; TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
; TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Whinston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/867,087B
; FILING DATE: June 2, 1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/323,449
; FILING DATE: October 14, 1994
; APPLICATION NUMBER: U.S. 08/485,981
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan. E.
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 4630-47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-867-087B-13

Query Match 34.5%; Score 428.5; DB 2; Length 250;
Best Local Similarity 40.4%; Pred. No. 2.1e-35;
Matches 95; Conservative 44; Mismatches 73; Indels 23; Gaps 4;

QY 16 IGRGKIEIKRIENTNRQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGRLYEYANN 75
Db 1 MGRGRVELKRIENKINRQVTFCKRRNGLLKKAYELSVLCDAEVALIIFSKRGLYEFGSA 60
QY 76 SVRGTIERYKKACSDAVNPPTITEANTQYQQEASKLRQIRDIONLNRHILGSLGSLN 135
Db 61 GITKLERYOHCYNQADSNAL-SETQSWYHEMSKLKAKFEALQRTQRHLLGEDLGPLS 119
QY 136 FKELNLESLERKIGISRVRSKKHEMLVAEIEYMQKREIELQNDNMYLSKI-----TERT 190
Db 120 VKELOLEKOLECALSQARQKTKQLMMEQVEELRRKROGLGEINRQKHKLEVEGSTSNY 179
QY 191 GLOQQESSVIHQGVYESGVTSSHQSGQYNRNYIAVNLLEPNQNSNQDQPPLQL 245
Db 180 RAMQQAQSWA--QGAVVENG-----AAYVQPPPHSAAMDSEPTLQI 217

RESULT 13
US-08-592-214A-8
; Sequence 8, Application US/08592214A
; Patent No. 5811536
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Cauliflower Floral Meristem Identify
; TITLE OF INVENTION: Genes and Methods of Using Same
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,214A
; FILING DATE: 26-JAN-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1927
; TELECOMMUNICATION INFORMATION:
```

QY 16 IGRKIEIKRIENTNRQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGRLEYANN 75  
:|::|||:|::|||:|::|||:|::|||:|::|||:|::|||:|::|||:|::|||:|::|||:

Db 1 MGRGVQLKRIENKINRQVTFSKRRNGLLKAHEISVLCDAEVAVIVFSPKGKLYEYATD 60  
QY 76 SVRGTI-----ERYKKACSDAVNPPTITEANTQYYQOEASKLRRQIRDIQNLRHILGESL 131  
Db 61 SRMDKILERYERYSYAEKALISAESSEGN---WCHERYKILKAKIETIQKCHKHLMGEDL 117  
QY 132 GSLNFKELKNLESRLKGISRVRSKKHEMLVAEIEYMQKREIELOQNDNMYLRSKITER-- 189  
Db 118 ESLNPKLEQLEQQLDSSLKHRSKSHLMAESISELQKKERSLOEENKALQKELAERQK 177  
QY 190 ---TGLQQQESSVIHQGTVESGVTSSHQS-----QYNNRN 222  
Db 178 AVASRQQQQQQQVWDQOOTHAAQATSSSSSFMMRQDQQGLPPPHNICFPPLTMGDRGEE 237  
QY 223 YIAVNILLEPNQNSSNQDQPPLQL 245  
Db 238 LAAAAAAQQQQPLPGQAQPOLRI 260

Search completed: January 27, 2003, 12:46:50  
Job time : 14.4453 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 27, 2003, 12:42:28 ; Search time 25.8947 Seconds  
(without alignments)  
1957.448 Million cell updates/sec

Title: US-09-978-382A-6  
Perfect score: 1242  
Sequence: 1 MEGGASNEVAESSKIGRGK.....NLEPNQNSSNQDPPPLQLV 246

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL\_21.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match % | Length | ID        | Description        |
|------------|-------|---------------|--------|-----------|--------------------|
| 1          | 1002  | 80.7          | 249    | 10 Q9AXZ1 | Q9axz1 brassica na |
| 2          | 845   | 68.0          | 244    | 10 Q9XHM3 | Q9xhm3 liquidambar |
| 3          | 829   | 66.7          | 225    | 10 Q93XH4 | Q93xh4 vitis vinif |
| 4          | 806   | 64.9          | 249    | 10 Q9MBE2 | Q9mbe2 rosa rugosa |
| 5          | 801   | 64.5          | 242    | 10 Q8VWZ3 | Q8vwz3 malus domes |
| 6          | 775   | 62.4          | 247    | 10 Q40900 | Q40900 petunia int |
| 7          | 771   | 62.1          | 247    | 10 Q08711 | Q08711 petunia hyb |
| 8          | 768   | 61.8          | 242    | 10 Q9LEP2 | Q9lep2 betula verr |
| 9          | 767   | 61.8          | 242    | 10 Q9ZTV9 | Q9ztv9 corylus ave |
| 10         | 763.5 | 61.5          | 264    | 10 Q9ZS30 | Q9zs30 gerbera hyb |
| 11         | 763   | 61.4          | 246    | 10 Q9ZS29 | Q9zs29 gerbera hyb |
| 12         | 759   | 61.1          | 246    | 10 Q9XFM8 | Q9xfm8 antirrhinum |
| 13         | 746.5 | 60.1          | 239    | 10 Q8RVW5 | Q8rvw5 phalaenopsi |
| 14         | 746.5 | 60.1          | 241    | 10 Q65111 | Q65111 populus tri |
| 15         | 742.5 | 59.8          | 239    | 10 Q41195 | Q41195 antirrhinum |
| 16         | 738.5 | 59.5          | 228    | 10 Q9ZPK9 | Q9zpk9 hyacinthus  |

|    |       |      |     |           |                    |
|----|-------|------|-----|-----------|--------------------|
| 17 | 738.5 | 59.5 | 248 | 10 Q41352 | Q41352 silene lati |
| 18 | 735   | 59.2 | 244 | 10 Q8RVK1 | Q8rvk1 gossypium h |
| 19 | 724   | 58.3 | 245 | 10 Q8VWZ2 | Q8vwz2 malus domes |
| 20 | 722   | 58.1 | 225 | 10 Q9SBK3 | Q9sbk3 cucumis sat |
| 21 | 719.5 | 57.9 | 238 | 10 Q65112 | Q65112 populus tri |
| 22 | 718.5 | 57.9 | 248 | 10 Q9ZRH4 | Q9zrh4 rosa hybrid |
| 23 | 716.5 | 57.7 | 236 | 10 Q9ARE9 | Q9are9 cucumis sat |
| 24 | 712.5 | 57.4 | 248 | 10 Q9MBE1 | Q9mbe1 rosa rugosa |
| 25 | 710   | 57.2 | 229 | 10 Q64959 | Q64959 cucumis sat |
| 26 | 709   | 57.1 | 237 | 10 Q9SBK1 | Q9sbk1 cucumis sat |
| 27 | 709   | 57.1 | 262 | 10 Q64958 | Q64958 cucumis sat |
| 28 | 705.5 | 56.8 | 254 | 10 Q43422 | Q43422 cucumis sat |
| 29 | 702   | 56.5 | 249 | 10 Q9MBE0 | Q9mbe0 rosa rugosa |
| 30 | 701.5 | 56.5 | 250 | 10 Q9MBD9 | Q9mbd9 rosa rugosa |
| 31 | 700.5 | 56.4 | 236 | 10 Q40704 | Q40704 oryza sativ |
| 32 | 700.5 | 56.4 | 247 | 10 Q9AWJ2 | Q9awj2 oryza sativ |
| 33 | 699.5 | 56.3 | 254 | 10 Q9SBK2 | Q9sbk2 cucumis sat |
| 34 | 695.5 | 56.0 | 253 | 10 Q42457 | Q42457 rumex aceto |
| 35 | 695   | 56.0 | 249 | 10 Q9SBR4 | Q9sbt4 fragaria an |
| 36 | 690   | 55.6 | 208 | 10 Q948V3 | Q948v3 magnolia pr |
| 37 | 686   | 55.2 | 221 | 10 Q9LQK1 | Q9lqk1 cucumis sat |
| 38 | 681   | 54.8 | 234 | 10 Q8RU44 | Q8ru44 hordeum vul |
| 39 | 674   | 54.3 | 215 | 10 Q93XE3 | Q93xe3 cucumis sat |
| 40 | 672.5 | 54.1 | 228 | 10 Q40882 | Q40882 petunia hyb |
| 41 | 656   | 52.8 | 259 | 10 Q24009 | Q24009 zea mays (m |
| 42 | 653.5 | 52.6 | 232 | 10 Q8RU43 | Q8ru43 hordeum vul |
| 43 | 652   | 52.5 | 225 | 10 Q43616 | Q43616 petunia hyb |
| 44 | 650.5 | 52.4 | 222 | 10 Q9ZTY6 | Q9zty6 pinus resin |
| 45 | 649.5 | 52.3 | 222 | 10 Q9S719 | Q9s719 picea maria |

## ALIGNMENTS

## RESULT 1

|        |                                                                       |                                         |              |      |         |
|--------|-----------------------------------------------------------------------|-----------------------------------------|--------------|------|---------|
| Q9AXZ1 | ID                                                                    | Q9AXZ1                                  | PRELIMINARY; | PRT; | 249 AA. |
| AC     | Q9AXZ1;                                                               |                                         |              |      |         |
| DT     | 01-JUN-2001                                                           | (TREMBlrel. 17, Created)                |              |      |         |
| DT     | 01-JUN-2001                                                           | (TREMBlrel. 17, Last sequence update)   |              |      |         |
| DT     | 01-MAR-2002                                                           | (TREMBlrel. 20, Last annotation update) |              |      |         |
| DE     | SHATTERPROOF1.                                                        |                                         |              |      |         |
| GN     | BNSHP1.                                                               |                                         |              |      |         |
| OS     | Brassica napus (Rape).                                                |                                         |              |      |         |
| OC     | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;    |                                         |              |      |         |
| OC     | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; |                                         |              |      |         |
| OC     | eurosid2 II; Brassicales; Brassicaceae; Brassica.                     |                                         |              |      |         |
| OX     | NCBI_TaxID=3708;                                                      |                                         |              |      |         |
| RN     | [1]                                                                   |                                         |              |      |         |
| RP     | SEQUENCE FROM N.A.                                                    |                                         |              |      |         |
| RC     | STRAIN=CV. BRIDGER;                                                   |                                         |              |      |         |
| RA     | Pylatuik J.D., Davis A.R., Bonham-Smith P.C.;                         |                                         |              |      |         |
| RT     | "Molecular cloning and characterization of a B. napus SHP1 gene.";    |                                         |              |      |         |
| RL     | Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.               |                                         |              |      |         |
| RN     | [2]                                                                   |                                         |              |      |         |
| RP     | SEQUENCE FROM N.A.                                                    |                                         |              |      |         |
| RA     | Pylatuik J.D., Davis A.R., Bonham-Smith P.C.;                         |                                         |              |      |         |
| RT     | "Isolation of the coding region of BnSHP by RT-PCR.";                 |                                         |              |      |         |
| RL     | Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.               |                                         |              |      |         |
| CC     | -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).                    |                                         |              |      |         |
| CC     | -!- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.   |                                         |              |      |         |
| DR     | EMBL; AF226865; AAK00646.1; -.                                        |                                         |              |      |         |
| DR     | EMBL; AY036062; AAK62033.1; -.                                        |                                         |              |      |         |
| DR     | HSSP; P11746; INNM.                                                   |                                         |              |      |         |
| DR     | InterPro; IPR002487; TF_Kbox.                                         |                                         |              |      |         |
| DR     | InterPro; IPR002100; TF_MADSbox.                                      |                                         |              |      |         |
| DR     | Pfam; PF01486; K-box; 1.                                              |                                         |              |      |         |
| DR     | Pfam; PF00319; SRF-TF; 1.                                             |                                         |              |      |         |
| DR     | PRINTS; PRO0404; MADSDOMAIN.                                          |                                         |              |      |         |
| DR     | SMART; SM00432; MADS; 1.                                              |                                         |              |      |         |
| DR     | PROSITE; PS00350; MADS_BOX_1; 1.                                      |                                         |              |      |         |
| DR     | PROSITE; PS50066; MADS_BOX_2; 1.                                      |                                         |              |      |         |
| KW     | DNA-binding; Nuclear protein; Transcription regulation.               |                                         |              |      |         |

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SQ SEQUENCE 249 AA; 28219 MW; BE78E063E1F5FB4E CRC64;
Query Match 80.7%; Score 1002; DB 10; Length 249;
Best Local Similarity 82.7%; Pred. No. 1.8e-62;
Matches 205; Conservative 17; Mismatches 22; Indels 4; Gaps 3;

QY 2 EGGASNEVAESSKIGRGKIEIKRIENTTNRQVTFCKRRNGLLKAYELSVLCDAEVALV 61
Db 3 EGGSSHD-AESSKIGRGKIEIKRIENTTNRQVTFCKRRNGLLKAYELSVLCDAEVALV 61

QY 62 IFSTRGLRYEYANNSVGRGTYERYKKACSDAVNPPTITEANTQYQOEASKLRRQIRDION 121
Db 62 IFSTRGLLYEYASNVKGTIERYKKACSDAVNPPTVTEANTKHYQOEASKLRRQIRDION 121

QY 122 LNRHILGESLGNFKELKNLESRLKIGISRVRSKKHMLVAIEIYMQKREIELONDNM 181
Db 122 SNRHIVGESLGNFKELKNLEGRLEKIGISRVRSKKSELLVAIEIYMQKREIMELQHVNM 181

QY 182 LRSKITE--RRGLQOESSVIHQGTVYESGVTSSH-QSGQYNNRYIAVNLLPEPNQSSNQ 238
Db 182 LRAKIEGARLNPEQHGSGVIGTAVYESGLSSSHDQSHYNNRYPVNLLEPNQOFSQ 241

QY 239 DQPLQLV 246
Db 242 DQPLQLV 249

RESULT 2
Q9XHM3 PRELIMINARY; PRT; 244 AA.
AC Q9XHM3;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Agamous homolog (Fragment).
GN LAG.
OS Liquidambar styraciflua (Amberboom) (Sweetgum tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Saxifragales; Hamamelidaceae; Liquidambar.
OX NCBI_TaxID=4400;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu J., Huang Y., Ding B., Tauer C.G.;
RT "cDNA cloning and expression of a sweetgum gene that shows homology
RT with Arabidopsis AGAMOUS.";
RL Plant Sci. 142:73-82(1999).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL; AF103903; AAD38119.1; -.
DR HSSP; P11746; 1MNN.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.
FT NON_TER 1
SQ SEQUENCE 244 AA; 28205 MW; A7BF0F928D52EAA8 CRC64;

Query Match 68.0%; Score 845; DB 10; Length 244;
Best Local Similarity 71.1%; Pred. No. 1.5e-51;
Matches 172; Conservative 30; Mismatches 32; Indels 8; Gaps 4;

QY 6 SNEVAESSKIGRGKIEIKRIENTTNRQVTFCKRRNGLLKAYELSVLCDAEVALVIFST 65
Db 10 SSEGSSSQKMGKRGKIEIKRIENTTNRQVTFCKRRNGLLKAYELSVLCDAEVALVIFSS 69

QY 66 RGRLEYEYANNSVGRGTYERYKKACSDAVNPPTITEANTQYQOEASKLRRQIRDIONLRH 125
Db 66 RGRLEYEYANNSVGRGTYERYKKACSDAVNPPTITEANTQYQOEASKLRRQIRDIONLRH 125
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Db 70 RGRLEYEYANNSVKSTIERYKKA-SDTSNPGSVSETNAOFYQQESSKLRQRIRDIONLRH 128
QY 126 ILGESLGNFKELKNLESRLKIGISRVRSKKHMLVAIEIYMQKREIELONDNMYLRSK 185
Db 129 IMGEALSLTFRELKNLEGRLEKIGISRVRSKKNELLFABIEIYMQKREIELQANMYLRAS 188
QY 186 ITERTGLQOESESVIHQGTVYESGVTSSHQSGQYNNRYIAVNILLE-PNQNSSNQDQPLQ 244
Db 189 IAEERNQQQ--TELMPGSVYETMPSSQ---PYDRSEFLVANLLEPPNHHYSRQDQTPLO 242
QY 245 LV 246
Db 243 LV 244

RESULT 3
Q93XH4 PRELIMINARY; PRT; 225 AA.
AC Q93XH4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE MAD-box transcription factor.
GN MADS1.
OS Vitis vinifera (Grape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitaceae;
OC Vitis.
OX NCBI_TaxID=29760;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-CV. SHIRAZ; TISSUE=FLOWER, AND FRUIT;
RX MEDLINE=21307190; PubMed=1414613;
RA Boss P.K., Vivier M., Matsumoto S., Dry I.B., Thomas M.R.;
RT "A cDNA from grapevine (Vitis vinifera L.), which shows homology to
RT AGAMOUS and SHATPERPROOF, is not only expressed in flowers but also
RT throughout berry development.";
RL Plant Mol. Biol. 45:541-553(2001).
DR EMBL; AF265562; AAK58564.1; -.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR PROSITE; PS00350; MADS_BOX_1; UNKNOWN_1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
SQ SEQUENCE 225 AA; 26151 MW; 509B50DFF92A5503 CRC64;

Query Match 66.7%; Score 829; DB 10; Length 225;
Best Local Similarity 72.3%; Pred. No. 1.8e-50;
Matches 167; Conservative 26; Mismatches 32; Indels 6; Gaps 2;

QY 16 IGRGKIEIKRIENTTNRQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGLRYEYANN 75
Db 1 MGRGKIEIKRIENTTNRQVTFCKRRNGLLKAYELSVLCDAEVALVIFSSRGLRYEYANN 60
QY 76 SVRGTYERYKKACSDAVNPPTITEANTQYQOEASKLRRQIRDIONLRHILGESLGN 135
Db 61 SVRTTIERYKKVCSDSNTSGVSEANAQFYQOEASKLRRQIRDIONLRHILGEALSSLN 120
QY 136 FKELKNLESRLKIGISRVRSKKHMLVAIEIYMQKREIELONDNMYLRSKITERTGLOQQ 195
Db 121 FKELKNLETRLEKIGISRVRSKKNELLFABIEIYMQKREIELQNSLFLRAQTAENERAQQ 180

QY 196 ESSVIHQGTVYESGVTSSHQSGQYNNRYIAVNLLPEPNQSSNQDQPLQLV 246
Db 181 MN--LMPGSQYESVPQPFYDS---QNLPLVNLDPNHHYSRHDQALQLV 225

RESULT 4
Q9MBE2 PRELIMINARY; PRT; 249 AA.
ID Q9MBE2
AC Q9MBE2;
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DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE MADS-box protein.
GN MASAKO D1.
OS Rosa rugosa (Rugosa rose).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.
OX NCBI_TaxID=74645;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FLOWER;
RX PubMed=10808068;
RA Kitahara K., Matsumoto S.;
RT "Rose MADS-box genes 'MASAKO C1 and D1' homologous to class C floral
RT identity genes.";
RL Plant Sci. 151:121-134(2000).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL: AB025643; BAA90743.1; -.
DR HSP: P11746; 1NMN.
DR InterPro: IPR002487; TF_Kbox.
DR InterPro: IPR002100; TF_MADSbox.
DR Pfam: PF01486; K-box; 1.
DR Pfam: PF00319; SRF-TF; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS0066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 249 AA; 28796 MW; 16F5AC7857C17803 CRC64;

Query Match 64.9%; Score 806; DB 10; Length 249;
Best Local Similarity 67.1%; Pred. No. 8e-49;
Matches 167; Conservative 29; Mismatches 37; Indels 16; Gaps 5;

QY 5 ASNEVAESSKKIGRGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVALVIFS 64
Db 10 ADPPSSQKKLGRGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVALVIFS 69
QY 65 TRGRLEYANNVSRGTIERYKKACSDAVNPPTITEANTQYQOEASKLRQIRDIONLNR 124
Db 70 TRGRLEYANNVSRGTIERYKKAC-DSSNTGSGVTETNVQFYQOEASKLRQIRDIONLNR 128
QY 125 HILGESLGNFKELKNLESRLKGISRVRSKKHEMLVAEIEYMQKREIQLNDNMVLR 184
Db 129 HILGEALSTLVNKLKLEGRLEKGISRSKKNEMLFAEIEYMQKREIQLQNHNNFLRA 188
QY 185 KITERGLQOQESSVIHQGTVYESGVTSSTSHQSG-----QYNNRYIAVNLLEPNQ--SSN 237
Db 189 KIAENDRAQOQOANMM-----PGTLSAYDQSMPPPPQSYDRSFLPV-ILESNNHHYNRQ 240
QY 238 QDQPPQLQV 246
Db 241 QNQTPLQLV 249

RESULT 5
Q8VWZ3
ID Q8VWZ3 PRELIMINARY; PRT; 242 AA.
AC Q8VWZ3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE C-type MADS box protein.
GN MADS14.
OS Malus domestica (Apple) (Malus sylvestris).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Maloideae; Malus.
OX NCBI_TaxID=3750;
RN [1]
```

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RP SEQUENCE FROM N.A.
RC TISSUE=VEGETATIVE GROWING POINT;
RA van der Linden C.G.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=VEGETATIVE GROWING POINT;
RA Vosman B., Smulders M.J.M.;
RT "Isolation of apple B- and C-type MADS box genes from vegetative
RT tissue.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ251117; CAC80857.1; -.
DR InterPro: IPR002487; TF_Kbox.
DR InterPro: IPR002100; TF_MADSbox.
DR Pfam: PF01486; K-box; 1.
DR Pfam: PF00319; SRF-TF; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; UNKNOWN_1.
DR PROSITE: PS0066; MADS_BOX_2; 1.
SQ SEQUENCE 242 AA; 27976 MW; 600B2A3595A37649 CRC64;

Query Match 64.5%; Score 801; DB 10; Length 242;
Best Local Similarity 67.5%; Pred. No. 1.7e-48;
Matches 164; Conservative 30; Mismatches 43; Indels 6; Gaps 2;

QY 6 SNEVAESS--KKIGRGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVALVIF 63
Db 4 ANQAPESSTQKKLGRGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVALVIF 63
QY 64 STRGRLEYANNVSRGTIERYKKACSDAVNPPTITEANTQYQOEASKLRQIRDIONL 123
Db 64 STRGRLEYANNVSRATIDRYKKACADSDTGGSVSEANTQFYQOEASKLRQIREION 123
QY 124 RHILGESLGNFKELKNLESRLKGISRVRSKKHEMLVAEIEYMQKREIQLNDNMVLR 183
Db 124 RHILGESLSTLVKELKNLEGRLEKGISRSKKNELFSEIEFQKRETELQHNHNNFLR 183
QY 184 SKITERGLQOQESSVIHQGTVYESGVTSSTSHQSGQYNNRYIAVNLLEPNQSSNODQPPL 243
Db 184 AKTAESEREQQOQTHMTPGTSYD---PSMPSNSYDRNFFPVILESNHHYPRQGQTAL 239
QY 244 QLV 246
Db 240 QLV 242

RESULT 6
Q40900
ID Q40900 PRELIMINARY; PRT; 247 AA.
AC Q40900;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Agamous protein.
GN PAGL1.
OS Petunia integrifolia (Violet-flowered petunia) (Petunia inflata).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
OX NCBI_TaxID=4103;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PISTIL;
RA Karunanandaa B., Kao T.-h.;
RT "Characterization of a flower-specific cDNA of Petunia inflata
RT encoding a putative homolog of Agamous protein.";
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL: L33973; AAA68001.1; -.
DR HSP: P11746; 1NMN.
DR TRANSFAC: T03126; -.
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Db 134 ELNFKELKNLEIKLEKGINKIRSKKNELLFAEIEYMQKREAEHLNHNQILRAKIAENE-R 192
QY 193 QQOESSVIHQGTVYESGVTSSHQSGQYNNRYIAVNLLEPNQNSNQDQPLQLV 246
Db 193 NQONLNVMPGGNGYELMQSQSYDS----RTYFQVDALQPNHHYPRQDQIPLQLV 242

RESULT 9
Q92TV9
ID Q92TV9 PRELIMINARY; PRT; 242 AA.
AC Q92TV9;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE MADS1.
GN MADS1.
OS Corylus avellana (European hazel).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fagales; Betulaceae; Corylus.
OX NCBI_TaxID=13451;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=99084765; PubMed=9869420;
RA Rigola D., Pe M.E., Fabrizio C., Me G., Sari-Gorla M.;
RT "CAMADS1, a MADS box gene expressed in the carpel of hazelnut.";
RL Plant Mol. Biol. 38:1147-1160(1998).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL; AF027376; AAD03486.1; -.
DR HSSP; P11746; 1MNM.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 2.
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 242 AA; 28023 MW; 6D74CD8654A1B719 CRC64;

Query Match 61.8%; Score 767; DB 10; Length 242;
Best Local Similarity 65.8%; Pred. No. 4.1e-46;
Matches 154; Conservative 34; Mismatches 40; Indels 6; Gaps 3;

QY 14 KKIGRGKIEIKRIENTTNRQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLYEYA 73
Db 14 RKLGRGKIEIKRIENTTNRQVTFCKRRNGLLKAYELSVLCDAEIALIVFSRGRLYEYA 73

QY 74 NN-SVRGTIERYKKACSDAVNPPTITEANTQYQQEASKLRRIQIRDIQNLRHILGESLG 132
Db 74 NNSSVKTIERYKKACADSSNSGVSSEANTQFYQQEAAKLGRQIRSVQDSNRHMLGEALS 133

QY 133 SLNFKELKNLESRLKIGISVRSKKHEMLVAEIEYMQKREIEQLQNDNMVYLSRKITERGL 192
Db 134 ELNFKELKNLEKGINRIRSKKNELLAEIEYMHKREVDLHNNQFLRAKIAENE-R 192

QY 193 QQOESSVIHQGTVYESGVTSSHQSGQYNNRYIAVNLLEPNQNSNQDQPLQLV 246
Db 193 NQONLNVMPGGNGYELMQSQSFDS----RNYFQVDALQPNHHYPRQDQMALQLV 242

RESULT 10
Q92S30
ID Q92S30 PRELIMINARY; PRT; 264 AA.
AC Q92S30;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE MADS-box protein, GAGAL.
GN GAGAL.
OS Gerbera hybrida.
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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Asterales; Asteraceae; Mutisieae; Gerbera.
OX NCBI_TaxID=18101;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=CV, TERRA REGINA;
RX MEDLINE=99168221; PubMed=10069067;
RA Yu D., Kotilainen M., Poelinen E., Mehto M., Elomaa P.,
RA Helariutta Y., Albert V.A., Teeri T.H.;
RT "Organ identity genes and modified patterns of flower development in
RT Gerbera hybrida (Asteraceae).";
RL Plant J. 17:51-62(1999).
DR EMBL; AJ009722; CAA08800.1; -.
DR HSSP; P11746; 1MNM.
DR TRANSFAC; T04587; -.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
SQ SEQUENCE 264 AA; 30413 MW; 9930224484335798 CRC64;

Query Match 61.5%; Score 763.5; DB 10; Length 264;
Best Local Similarity 64.6%; Pred. No. 7.9e-46;
Matches 153; Conservative 34; Mismatches 43; Indels 7; Gaps 3;

QY 14 KKIGRGKIEIKRIENTTNRQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLYEYA 73
Db 31 RKMKGKIEIKRIENTTNRQVTFCKRRNGLLKAYELSVLCDAEVALVIFSRGRLYEYA 90

QY 74 NNSVRGTIERYKKACSDAVNPPTITEANTQYQQEASKLRRIQIRDIQNLRHILGESLG 129
Db 91 NNSVKTIDYKKACLDPPPTSGTVAEANTQYQQEAAKLROQIANLQNRQFYRNIMGE 150

QY 130 SLGSLNFKELKNLESRLKIGISVRSKKHEMLVAEIEYMQKREIEQLQNDNMVYLSRKITER 189
Db 151 SLGDMVPKDLNLEKLEKAIKIRAKKNELLFAEIEYMQKRELEHNSNQFLRAKIVEN 210

QY 190 TGLQQOESSVIHQGTVYESGVTSSHQSGQYNNRYIAVNLLEPNQNSNQDQPLQLV 246
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RESULT 11
Q92S29
ID Q92S29 PRELIMINARY; PRT; 246 AA.
AC Q92S29;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE MADS-box protein, GAGA2.
GN GAGA2.
OS Gerbera hybrida.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Asterales; Asteraceae; Mutisieae; Gerbera.
OX NCBI_TaxID=18101;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=CV, TERRA REGINA;
RX MEDLINE=99168221; PubMed=10069067;
RA Yu D., Kotilainen M., Poelinen E., Mehto M., Elomaa P.,
RA Helariutta Y., Albert V.A., Teeri T.H.;
RT "Organ identity genes and modified patterns of flower development in
RT Gerbera hybrida (Asteraceae).";
RL Plant J. 17:51-62(1999).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL; AJ009723; CAA08801.1; -.
DR HSSP; P11746; 1MNM.
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DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Agamous homolog.
GN PRAG1.
OS Populus trichocarpa (Western balsam poplar).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Malpighiales; Salicaceae; Populus.
OX NCBI_TaxID=3694;
RN [1]
RP SEQUENCE FROM N.A.
RA Brunner A.M., Rottmann W.H., Sheppard L.A., Strauss S.H.;
RT "Two Populus trichocarpa genes homologous to AGAMOUS.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL; AF052570; AAC06237.1; -.
DR HSSP; P11746; 1MN.
DR INTERPRO; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00666; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 241 AA; 27559 MW; 4C2BFD1F29E99CF CRC64;

Query Match 60.1%; Score 746.5; DB 10; Length 241;
Best Local Similarity 63.2%; Pred. No. 1.1e-44;
Matches 153; Conservative 41; Mismatches 41; Indels 7; Gaps 3;

QY 7 NEVAESS--KKIGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVALVIFS 64
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QY 65 TRGLYEYANNVSRGTIERKKACSDAVNPPTITEANTQYYQQEASKLRQIRDIQNLR 124
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QY 125 HILGESLGNLFKELKNLESRLKGISRVRSKKHEMLVAEIEYMKREIELQNDNMYLRS 184
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QY 185 KITERTGLQQQESSVIHQCTVYESGVTSSHQSGQYNNRYIAVNLLLEPNQNSNODOPPLQ 244
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QY 245 LV 246
DB 240 LV 241

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DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Ple protein.
GN PLE.
OS Antirrhinum majus (Garden snapdragon).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Veroniceae; Antirrhinum.
OX NCBI_TaxID=4151;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93137332; PubMed=8093684;
RA Bradley D., Carpenter R., Sommer H., Hartley N., Coen E.;
RT "Complementary floral homeotic phenotypes result from opposite
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RT orientations of a transposon at the plena locus of Antirrhinum.";
RL Cell 72:85-95(1993).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL; S53900; AAB25101.1; -.
DR HSSP; P11746; 1MN.
DR TRANSFAC; T03130; -.
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DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR PRINTS; PR00319; SRF-TF; 1.
DR SMART; SM00404; MADSDOMAIN.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00666; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 239 AA; 27662 MW; D48C6C18043F9682 CRC64;

Query Match 59.8%; Score 742.5; DB 10; Length 239;
Best Local Similarity 63.1%; Pred. No. 2e-44;
Matches 152; Conservative 38; Mismatches 44; Indels 7; Gaps 3;

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QY 67 GRLYEYANNVSRGTIERKKACSDAVNPPTITEANTQYYQQEASKLRQIRDIQNLRHI 126
DB 65 GRLYEYANNVSRGTIERKKASADSSNSVSTSEANTQFYQQEANKLRQIREIQTSNROM 124

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DB 185 AEGERAQQQMN--LMPGSDYQPMTSQSYDV----RNFPLMNLMEPNQQOQYSRHDQALQL 238

QY 246 V 246
DB 239 V 239

Search completed: January 27, 2003, 12:45:40
Job time : 26.8947 secs
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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 2, 2003, 06:06:04 ; Search time 42.9887 Seconds  
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Total number of hits satisfying chosen parameters: 882724

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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| 2          | 896   | 100.0       | 896    | 4  | US-09-349-677-5 Sequence 5, Appli    |
| 3          | 536.8 | 59.9        | 959    | 4  | US-09-067-800-7 Sequence 7, Appli    |
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| 5          | 344.8 | 38.5        | 1125   | 1  | US-08-460-512-6 Sequence 6, Appli    |
| 6          | 335.8 | 37.5        | 5622   | 4  | US-09-067-800-3 Sequence 3, Appli    |
| 7          | 335.8 | 37.5        | 5622   | 4  | US-09-349-677-3 Sequence 3, Appli    |
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| 9          | 312.6 | 34.9        | 1159   | 4  | US-09-410-464-14 Sequence 14, Appli  |
| 10         | 305.2 | 34.1        | 723    | 4  | US-09-410-464-11 Sequence 11, Appli  |
| 11         | 305.2 | 34.1        | 1219   | 4  | US-09-410-464-10 Sequence 10, Appli  |
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| 14         | 275.8 | 30.8        | 1457   | 1  | US-08-460-512-1 Sequence 1, Appli    |
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| 17         | 159   | 17.7        | 498    | 4  | US-09-073-587-6 Sequence 6, Appli    |
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| 19         | 149.2 | 16.7        | 1062   | 4  | US-09-105-652-1 Sequence 1, Appli    |
| 20         | 149.2 | 16.7        | 1062   | 4  | US-09-349-677-1 Sequence 1, Appli    |
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| 22         | 143.2 | 16.0        | 1345   | 3  | US-08-659-188-7 Sequence 7, Appli    |
| 23         | 143.2 | 16.0        | 1345   | 3  | US-08-655-227-7 Sequence 7, Appli    |
| 24         | 143.2 | 16.0        | 1345   | 3  | US-08-655-241-7 Sequence 7, Appli    |
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## ALIGNMENTS

RESULT 1  
US-09-067-800-5  
; Sequence 5, Application US/09067800  
; Patent No. 6198024  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin F.  
; APPLICANT: Ferrandiz, Cristina  
; TITLE OF INVENTION: Seed Plants Characterized by Delayed  
; TITLE OF INVENTION: Seed Dispersal  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/067,800  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UD 2948  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 896 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
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; LOCATION: 896  
; OTHER INFORMATION: /note= "There is a poly(A) tail at  
; OTHER INFORMATION: the end of the cDNA sequence."  
; FEATURE:  
; NAME/KEY: misc\_feature

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; LOCATION: 1..896
; OTHER INFORMATION: /note= "AGLI cDNA and deduced
; OTHER INFORMATION: protein sequences."
; US-09-067-800-5

Query Match 100.0%; Score 896; DB 4; Length 896;
Best Local Similarity 100.0%; Pred. No. 5.2e-266;
Matches 896; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-349-677-5
; Sequence 5, Application us/09349677
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; Patent No. 6288305
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Ferrandiz, Cristina
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/349,677
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/067,800
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 896 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 7..753
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 896
; OTHER INFORMATION: /note= "There is a poly(A) tail at
; OTHER INFORMATION: the end of the cDNA sequence."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..896
; OTHER INFORMATION: /note= "AGLI cDNA and deduced
; OTHER INFORMATION: protein sequences."
; US-09-349-677-5

Query Match 100.0%; Score 896; DB 4; Length 896;
Best Local Similarity 100.0%; Pred. No. 5.2e-266;
Matches 896; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATCAATGAGGAAGGTGGAGTAGTCAGCAGCAGAGAGTAGCAAGAACTAGGGAGA 60
Db 1 GGATCAATGAGGAAGGTGGAGTAGTCAGCAGCAGAGAGTAGCAAGAACTAGGGAGA 60
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RESULT 3

US-09-067-800-7  
; Sequence 7, Application US/09067800  
; Patent No. 6198024  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin F.  
; APPLICANT: Ferrandiz, Cristina  
; TITLE OF INVENTION: Seed Plants Characterized by Delayed  
; TITLE OF INVENTION: Seed Dispersal  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/067,800  
; FILING DATE:  
; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UD 2948  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 959 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 78..818  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 1..959  
; OTHER INFORMATION: /note= "AGL5 cDNA and deduced  
; OTHER INFORMATION: protein sequences."  
; US-09-067-800-7

Query Match 59.9%; Score 536.8; DB 4; Length 959;  
Best Local Similarity 82.1%; Pred. No. 1.7e-155;  
Matches 632; Conservative 0; Mismatches 132; Indels 6; Gaps 1;

QY 6 AATGGAGGAAGTGGGAGTAGTCACGACGAGAGAGTAGCAAGAACTAGGAGAGGGAA 65  
Db 77 AATGGAGGGTGGTGGAGTAATGAAGTAGCAGAGAGCAGCAAGAGATAGGAGAGGAA 136  
QY 66 AATAGAGATAAGAGGATAGAGAACACAAATCGTCAAGTTACTTTCTGCAACGACG 125  
Db 137 GATAGAGATAAAGAGGATAGAGAACACTACGAATCGTCAAGTCACTTTCTGCAACGACG 196  
QY 126 CAATGGTCTTCTCAAGAAAGCTTATGAACCTCTCTCTGTGTGTGATGCCGAAGTTGCCCT 185  
Db 197 CAATGGTCTTCTCAAGAAAGCTTATGAGCTCTCTCTGTGTGTGATGCCGAAGTTGCCCT 256  
QY 186 CGTCATCTTCTCCACTCGTGGCCGCTCTATGAGTACGCCAACACACAGTGTGAGGGGTAC 245  
Db 257 TGTCTATCTTCTCCACTCGAGGCCGCTCTACAGGATACGCCAACACAGTGTGAGAGGAAC 316  
QY 246 AATTCAAAAGGTACAAGAAAGCTTGTTCGATGCCGTCAACCTCTCTTCCGTCAACGAGC 305  
Db 317 AATAGAAAGGTACAAGAAAGCTTGTTCGACGCCGCTTAACCTTCGACCATCACCGAAGC 376  
QY 306 TAATACTCAGTACTATCAGCAAGAGCCCTCTAAGCTTCGGAGGAGATTCGAGATATTCA 365  
Db 377 TAATACTCAGTACTATCAGCAAGAGCCGCTCTAAGCTTCGGAGGAGATTCGAGATATTCA 436  
QY 366 GAATCAATAGGCATATTTGGGGAATCACTTTGGTTCCTTGAACCTTCAAGGAACTCAA 425  
Db 437 GAATTTGAACAGACACATTTCTTGGTGAATCTCTTGGTTCCTTGAACCTTTAAGGAACTCAA 496  
QY 426 AAACCTAGAAAGGAGCTCTTGAAGAAAGGAATCAGCGGTCTCCGCTCCAAAAAGAAATGAGCT 485  
Db 497 GAACCTTGAAGAGTAGGCTTTGAGAAAGGAATCAGTCTGCTCCGATCCAAAGAACGAGAT 556  
QY 486 GTTAGTGCAGAGATAGATATATGCAGAGAGGGAATGAATTCGGACCCAGAGTTGCAACACAATAACAT 545  
Db 557 GTTAGTGCAGAGATTAATACATACAAAAAGGAAATCGAGCTGCAAAAAACGATAACAT 616  
QY 546 GTACCTGGCAGAAAGATAGCCGAAGGCCAGATTGAATTCGGACCCAGCAGGAAATCGAG 605  
Db 617 GTATCTCCGCTCCCAAGATTACTGAA-----AGAACAGGTCTACAGCAACAGATCGAG 670  
QY 606 TGTATACAAGGACGACAGTTTACGAATCCGGTGTATCTTCTCATGACCAAGTCCGAGCA 665  
Db 671 TGTGATACATCAAGGGACAGTTTACGAGTGGGTGTTACTTTCTTCTTCCAGCAGTCGGGCA 730  
QY 666 TTATAATCGGAACCTATATTCGGGTGAACCTTCTTGAACCGAAATCAGCAATTTCTCCGGCCA 725

Db 731 GTATAACCGGAATTATATGCGGTAACTTCTTGAAACCGAATCAGAAATTCCTCCAACCA 790  
QY 726 AGACCAACCTCCTCTCAACTTGTGTAAGTCAAAACATGATAACTTGTGT 775  
Db 791 AGACCAACCACTCTGCAACTGTTGTTGATTCAGTCTAACATAAGCTTCTT 840

RESULT 4  
US-09-349-677-7  
; Sequence 7, Application US/09349677  
; Patent No. 6288305  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin F.  
; APPLICANT: Ferrandiz, Cristina  
; TITLE OF INVENTION: Seed Plants Characterized by Delayed  
; TITLE OF INVENTION: Seed Dispersal  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE:  
; APPLICATION NUMBER: US/09/349,677  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; FILING DATE:  
; APPLICATION NUMBER: 09/067,800  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UD 2948  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 959 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 78..818  
; NAME/KEY: misc feature  
; LOCATION: 1..959  
; OTHER INFORMATION: /note= "AGL5 cDNA and deduced  
; OTHER INFORMATION: protein sequences."  
US-09-349-677-7

Query Match 59.9%; Score 536.8; DB 4; Length 959;  
Best Local Similarity 82.1%; Pred. No. 1.7e-155;  
Matches 632; Conservative 0; Mismatches 132; Indels 6; Gaps 1;

QY 6 AATGGAGGAAGTGGGAGTAGTCACGACGACAGAGTAGCAAGAACTAGGAGAGGGAA 65  
Db 77 AATGGAGGTGTCGCGAGTAATGAAGTAGCAGAGAGCAAGAAAGATAGGAGAGGAA 136  
QY 66 AATAGATATAAGAGATAGAGAACACAAATCGTCAAGTTACTTCTGCAACGACG 125  
Db 137 GATAGATATAAGAGGATAGAGAACACTACGAATCGTCAAGTCACTTCTGCAACGACG 196

QY 126 CAATGGTCTTCTCAAGAAAGCTTATGAACCTCTCTGTCTTGTGTGATCCCGAAGTTGCCCT 185  
Db 197 CAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGTCTTGTGTGACGCTGAGGTTGCTCT 256  
QY 186 CGTCATCTTCTCCACTCGTGGCGTCTCTATGAGTAGCGCCACACACAGTGTGAGGGGTAC 245  
Db 257 TGTCTATCTTCTCCACTCGAGGCGTCTCTACAGTAGCCCAACACAGTGTGAGAGGAAC 316  
QY 246 AATTGAAAGGTACAAGAAAGCTTGTCCGATGCGGTCAAAACCTCTTCCGTCACCCGAAGC 305  
Db 317 AATAGAAAGGTACAAGAAAGCTTGTCTCGACGCGCTTAACCTCCGACCATCACCCGAGC 376  
QY 306 TAATACTCAGTACTATCAGCAAGAGCCTCTAAGCTTTCGGAGGCAGATTCGAGATATTCA 365  
Db 377 TAATACTCAGTACTATCAGCAAGAGGCGTCTAACTCCGGAGACAGATTCGGGACATTC 436  
QY 366 GAATTCAAATAGGCATATTGTTGGGGATCATTGGTTCCTTGAACCTCAAGGAACCTCAA 425  
Db 437 GAATTTGAACAGACACATCTTGGTGAATCTCTTGGTTCCTTGAACCTTAAAGGAACCTCAA 496  
QY 426 AAACCTAGAAGGACGCTTTGAAAAGGAATACGCCGTGTCGCTCCAAACCAAGTACGCT 485  
Db 497 GAACCTTGAAGTAGGCTTGAGAAAGGATCAGTCTGCTCCGATCCCAAGAGCAGAGAT 556  
QY 486 GTTAGTGGCAGAGATAGAGTATATGCAGAAAGGGAATGGAGTTGCAACACACATAACAT 545  
Db 557 GTTAGTTCGAGAGATTAATACATGCAAAAAGGGAAATCGAGCTGCAAAACGATACAT 616  
QY 546 GTACCTGGAGCAAGATAGCCGAAGGCGCCAGATTGAATCCGAGCCAGCAGGAATCGAG 605  
Db 617 GTATCTCCGCTCCAAGATTACTGAA-----AGAAACAGGTCTACAGCAACAAGAAATCGAG 670  
QY 606 TGTGATACAAAGGACGACAGTTTACGAATCCGGTGTATCTTCTCATGACCAGTCGCAGCA 665  
Db 671 TGTGATACATCAAGGACAGTTTACGAGTCGGGTGTTACTTCTCTCACCAGTCGGGGCA 730  
QY 666 TTATAATCGGAACATATATCCGGTGAACCTTCTTGAACCGAATCAGCAATTCCTCCGGCCA 725  
Db 731 GTATAACCGGAATTATATTGCGGTAACTTCTTGAACCGAATCAGAAATTCCTCCAACCA 790  
QY 726 AGACCAACCTCCTCTTCAACTTGTGTAACCTCAAAACATGATAACTTGTGT 775  
Db 791 AGACCAACCACTCTGCAACTTGTGTTGATTCAGTCTAACATAAGCTTCTT 840

RESULT 5  
US-08-460-512-6  
; Sequence 6, Application US/08460512  
; Patent No. 5744693  
; GENERAL INFORMATION:  
; APPLICANT: MEYEROWITZ, Elliot M.  
; APPLICANT: YANOFKY, Martin F.  
; APPLICANT: MA, Hong  
; TITLE OF INVENTION: PLANTS HAVING ALTERED FLORAL DEVELOPMENT  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Richard F. Trecartin  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/460,512  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/293,278

```

; FILING DATE:
; APPLICATION NUMBER: US/07/956,694
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-57322/RFT
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1125 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 110..853
;
US-08-460-512-6
Query Match 38.5%; Score 344.8; DB 1; Length 1125;
Best Local Similarity 68.9%; Pred. No. 2.2e-96;
Matches 488; Conservative 0; Mismatches 217; Indels 3; Gaps 1;

QY 46 AAGAAATAGGAGAGGAGGAAATAGAGATAAGAGGATAGAGAACACAAATCGTCAA 105
Db 152 AGAAATCTGGAGAGGAGGAGATGAGATCAACGGATCGAAACACAAACGATCGTCAA 211
QY 106 GTTACTTCTGCAACGACGCAATGCTCTCAAGAAAGCTATGAACCTCTGTCTGTTG 165
Db 212 GTCACTTCTGCAAGAGACGCAATGTTTACTCAAAAGGCTATGAATATCTGTGCTC 271
QY 166 TGTGATCCGGAAGTTGCTCTCTCATCTTCTCCACTCGTGGCGTCTATGAGTAGGCC 225
Db 272 TGTGATCTGAGGTTGCTTGTATGTTCTCTCAAGCAGAGGCGAGCTCTATGAGTAGGCC 331
QY 226 AACACAGTGTGAGGGTACAAATTGAAGGTACAGAAAGCTTTCGATCCCGTCAAC 285
Db 332 AACACAGTGTGAAGCAACAATTGAGAGGTACAGAAAGCTTGTTCAGATTCTCTCAAC 391
QY 286 CTTCTTCCGTCACCGAAGCTTAATCTCAGTACTATCAGCAAGAAAGCTCTAAGCTTCGG 345
Db 392 ACTGGTCAATTTCCGAGGCCAATGCTCAGATATTATCAGCAAGAAAGCTCTCAACATCGC 451
QY 346 AGGCAGATTGAGATATTCAGAAATTCAGAAATAGGCATATGTTGGGAATCACTTGGTTCC 405
Db 452 GCACAAATGGAAATCTGCAGAAATCAGACAGGAAATGTTGGGTGAATCACTGGCTGCA 511
QY 406 TTGAATCTCAAGGAATCAAAACCTAGAGAGGACGCTTGAAGAAAGAAATCAGCCGTGTC 465
Db 512 CTGAGCTCAGAGATCTGAAGAAATCTGGAACAAAATTTGAAAAGGCAATTAGCAAAATC 571
QY 466 CGTCCAAAAGAAATGAGCTGTTAGTGGCAGAGATAGAGTATATGACAGAGGGAATG 525
Db 572 AGATCCAAAAGAAATGAGCTGCTGTTGCTGAAATTTGAGTACATGACAGAGGGAAT 631
QY 526 GAGTTCACACAAATTAACATGTACCTCGAGCAAGATAGCGGAGCGCGCAGATTTGAAT 585
Db 632 GATTACACACAAATCAGTACCTCGAGCAAGATTTGCTGAAGTGAAGTGAAGTGAAGT 688
QY 586 CCGGACACAGGAATTCGAGTGTGATACAGGGGACACAGTTTACGAATCCGGTGTATCT 645
Db 689 CAGCAGCAGCAGCAGCAGCAGATGAATGATGCCAGGAGTTCAAGCTATGAGCTT 748
QY 646 TCTCATGACCAAGTTCGAGCATTTAATCGAAGTATATTCGGGTGAACCTTCTTGAACCG 705
Db 749 GTGCTCCACCTCATCAATTTGATATCTCGAAACTATTACAAAGTTAATGGTTTGCAACC 808
QY 706 AATCAGCAATTCCTCGGCGCAAGCAACCTCTCTTCAACTTGTGTAA 753
Db 809 AACAACTATTACACTAGACAGACCAACCACTCTCTTCAACTAGTCTAA 856
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RESULT 6
US-09-067-800-3
; Sequence 3, Application US/09067800
; Patent No. 6198024
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Ferrandiz, Cristina
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/067,800
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5622 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..5622
; OTHER INFORMATION: /label= AGL1_promoter
; OTHER INFORMATION: /note= "Nucleotide sequence of the AGL1 promoter."
US-09-067-800-3
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Query Match 37.5%; Score 335.8; DB 4; Length 5622;
Best Local Similarity 99.4%; Pred. No. 2.8e-93;
Matches 337; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 558 AAAGATAGCGGAGCGCGCAGATTGAATCCGGACGACGAGGAATCGAGTGTGATACAAG 617
Db 5025 ATAGATAGCGGAGCGCGCAGATTGAATCCGGACGACGAGGAATCGAGTGTGATACAAG 5084
QY 618 GACGACAGTTTACGAATCCGGTGTATCTCTCATGACCAAGTCGAGCATTTAATCGGAA 677
Db 5085 GACGACAGTTTACGAATCCGGTGTATCTCTCATGACCAAGTCGAGCATTTAATCGGAA 5144
QY 678 CTATATTCGGGTGAACCTTCTTGAACCGGAATCAGCAATTTCTCCGSCCAAGACCACTCC 737
Db 5145 CTATATTCGGGTGAACCTTCTTGAACCGGAATCAGCAATTTCTCCGSCCAAGACCACTCC 5204
QY 738 TCTTCAACTTGTGTAACTCAAAACATGATAACTTGTTCCTCCCTCATACGATTAAAG 797
Db 5205 TCTTCAACTTGTGTAACTCAAAACATGATAACTTGTTCCTCCCTCATACGATTAAAG 5264
QY 798 GAGAGACGAGAGTTCATTTTATTTATATAACGCGACTGTGTATTCATAGTTTAGGTTTC 857
Db 5265 GAGAGACGAGAGTTCATTTTATTTATATAACGCGACTGTGTATTCATAGTTTAGGTTTC 5324
QY 858 TAATAATGATAATAACAAACAACTGTGTTTCTTTCTTCA 896
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Db 5325 TAATAATGATAATAACAAAACGTGTGTTCTTTTGCTTAA 5363

RESULT 7  
US-09-349-677-3

Patent No. 6288305  
GENERAL INFORMATION:  
APPLICANT: Yanofsky, Martin F.  
APPLICANT: Ferrandiz, Cristina  
TITLE OF INVENTION: Seed Plants Characterized by Delayed  
TITLE OF INVENTION: Seed Dispersal  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/349,677

|                       |        |                    |        |              |
|-----------------------|--------|--------------------|--------|--------------|
| Query Match           | 37.5%; | Score 335.8;       | DB 4;  | Length 5622; |
| Best Local Similarity | 99.4%; | Pred. NO. 2.8e-93; |        |              |
| Matches 337:          |        |                    |        |              |
| Conservative          | 0;     | Mismatches 2;      | Indels | 0;           |
| Gaps                  | 0;     |                    |        |              |

|    |      |                                                              |      |
|----|------|--------------------------------------------------------------|------|
| QY | 558  | AAAGATACCGCAAGCGCCAGATTGAATCGGACGACGAGGAATCGAGTGTGATACAAGG   | 617  |
|    |      |                                                              |      |
| Db | 5025 | ATAGATACCGCAAGCGCCAGATTGAATCGGACGACGAGGAATCGAGTGTGATACAAGG   | 5084 |
| QY | 618  | GAGCACAGTTTACGAATCCGGTGTATCTTCTCATGACCAAGTCGAGCATTATAATCGGAA | 677  |
|    |      |                                                              |      |
| Db | 5085 | GAGCACAGTTTACGAATCCGGTGTATCTTCTCATGACCAAGTCGAGCATTATAATCGGAA | 5144 |
| QY | 678  | CTATATTCGGGTGAACCTTCTTTGAACCGGAATCAGCAATTCCTCGGGCAAGCAACCTCC | 737  |
|    |      |                                                              |      |
| Db | 5145 | CTATATTCGGGTGAACCTTCTTTGAACCGGAATCAGCAATTCCTCGGGCAAGCAACCTCC | 5204 |
| QY | 738  | TCATTCAACTGTGTAACTCAAAACATGATAACTTGTTCCTCCCTCATACGATTAAAGA   | 797  |
|    |      |                                                              |      |
| Db | 5205 | TCATTCAACTGTGTAACTCAAAACATGATAACTTGTTCCTCCCTCATACGATTAAAGA   | 5264 |



Db 520 GACTTGCACAACAATAACCAGCTTCTCCGAGCAAAAGATTGCAGAGAAATGAAGAAAGCGA 579  
QY 586 CCGGACCAGCA 596  
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Db 580 CAGCACATGAA 590  
| | | | |  
RESULT 9  
US-09-410-464-14  
; Sequence 14, Application US/09410464  
; Patent No. 6395892  
; GENERAL INFORMATION:  
; APPLICANT: Strauss et al.  
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in  
; TITLE OF INVENTION: poplar and other plant species.  
; FILE REFERENCE: 53375  
; CURRENT APPLICATION NUMBER: US/09/410,464  
; CURRENT FILING DATE: 1999-10-01  
; EARLIER APPLICATION NUMBER: 09/287,700  
; EARLIER FILING DATE: 1999-04-06  
; EARLIER APPLICATION NUMBER: 60/080,851  
; EARLIER FILING DATE: 1998-04-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 1159  
; TYPE: DNA  
; ORGANISM: Populus balsamifera subsp. trichocarpa  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (99)...(815)  
US-09-410-464-14

Query Match 34.9%; Score 312.6; DB 4; Length 1159;  
Best Local Similarity 73.0%; Pred. No. 1.8e-86;  
Matches 402; Conservative 0; Mismatches 149; Indels 0; Gaps 0;  
QY 46 AAGAACTAGGAGAGGAAATAGAGATAAAGAGGATAGAGAACACAAATCGTCAA 105  
| | | | |  
Db 138 AGGAAGCTGGGAGGGAAGGTGGAGATCAAGGGATCGAGAACACCACCATCGCCAA 197  
| | | | |  
QY 106 GTTACTTTCTGCAACGACGCAATGGTCTCTCAAGAAAGCTTATGAACTCTCTGTCTG 165  
| | | | |  
Db 198 GTCACTTTCTGCAAAAGCGGAATGGTTGCTCAAGAAAGCCATGATTAATCTGTTCTT 257  
| | | | |  
QY 166 TGTGATGCGGAAGTTGCCCTCGCTCATCTCTCCACTCGTGGCGTCTCTATGAGTACGCC 225  
| | | | |  
Db 258 TGCATGCTGAGGTGCACTCATCTCTCCAGCGGTGGAGCCCTTATGAGTACTCT 317  
| | | | |  
QY 226 AACACAGTGTGAGGGGTACAATTGAAAGGTACAAGAAAGCTTGTTCGGATGCCGTCAAC 285  
| | | | |  
Db 318 AACAAAGTGTCAAATCTCAAATGAAAGGTACAAAAGGCATCTGCAGATTCTTCCAAC 377  
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QY 286 CCTCCTTCGTCACCGAAGCTAATACTAGTACTATCAGCAAGAACCTCTAAGCTTCGG 345  
| | | | |  
Db 378 AACGGTTCAGTTTCTGAAGCCAATGCTCAGTTCTATCAGCAAGAAAGTCCAGCTGCGC 437  
| | | | |  
QY 346 AGGCAGATTCCAGATATTCAGAAATCAATAGGCATATGTTGGGGAATCACTTGGTTCC 405  
| | | | |  
Db 438 TCGCAAAATGGTAAATTCGAGAATTCAAACAGGAATATGCTGGTGAATCACTAGTGA 497  
| | | | |  
QY 406 TTGAACCTCAAGGAACCTCAAAACCTAGAGGAGCTCTTGAAGAAAGGAATCAGCCGTCTC 465  
| | | | |  
Db 498 TTGAGTGTGAAGGAACTTAAGAGCTTGGAGATAAACTTGAGAAAGGATTTGTAAGATT 557  
| | | | |  
QY 466 CGTCCCAAAAGAAATGAGCTGTAGTGGCAGAGATAGACTATATGCAGAAAGGGAATG 525  
| | | | |  
Db 558 CGTTGCAAAAGAAATGAGCTGTGTTGCTGAATTTGAGTATATGCAGAAAGGGAGATT 617  
| | | | |  
QY 526 GAGTTGCAACACAATAACATGTACTCGGAGCAAAAGATAGCCGAAGGCCAGATTGAAT 585  
| | | | |  
Db 618 GACTTGCAACAACAATAACAGCTTCTCCGAGCAAAAGATTGCAGAGAAATGAAGAAAGCGA 677  
| | | | |

QY 586 CCGGACCAGCA 596  
| | | | |  
Db 678 CAGCACATGAA 688  
| | | | |  
RESULT 10  
US-09-410-464-11  
; Sequence 11, Application US/09410464  
; Patent No. 6395892  
; GENERAL INFORMATION:  
; APPLICANT: Strauss et al.  
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in  
; TITLE OF INVENTION: poplar and other plant species.  
; FILE REFERENCE: 53375  
; CURRENT APPLICATION NUMBER: US/09/410,464  
; CURRENT FILING DATE: 1999-10-01  
; EARLIER APPLICATION NUMBER: 09/287,700  
; EARLIER FILING DATE: 1999-04-06  
; EARLIER APPLICATION NUMBER: 60/080,851  
; EARLIER FILING DATE: 1998-04-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 723  
; TYPE: DNA  
; ORGANISM: Populus balsamifera subsp. trichocarpa  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(723)  
US-09-410-464-11

Query Match 34.1%; Score 305.2; DB 4; Length 723;  
Best Local Similarity 73.2%; Pred. No. 2.7e-84;  
Matches 391; Conservative 0; Mismatches 143; Indels 0; Gaps 0;  
QY 46 AAGAACTAGGAGAGGAAATAGAGATAAAGAGGATAGAGAACACAAATCGTCAA 105  
| | | | |  
Db 40 AGGAAGCTGGGAGGGAAGGTGGAGATCAAGCGGATCGAGAACACCACCATCGCCAA 99  
| | | | |  
QY 106 GTTACTTTCTGCAACGACGCAATGGTCTCTCAAGAAAGCTTATGAACTCTCTGTCTTG 165  
| | | | |  
Db 100 GTCATTTCTGCAAAAGCGCAGTGGTTTGTCTCAAGAAAGCCATGCAATATATCTGTTCT 159  
| | | | |  
QY 166 TGTGATGCGGAAGTTGCCCTCGCTCATCTCTCCACTCGTGGCGTCTCTATGAGTACGCC 225  
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Db 160 TGCATGCTGAGGTGCACTCATCTCTCTAGCCGCGGTGCGCTTATGAGTACTCT 219  
| | | | |  
QY 226 AACACAGTGTGAGGGGTACAATTGAAAGGTACAAGAAAGCTTGTTCGGATGCCGTCAAC 285  
| | | | |  
Db 220 AACGATAGTCAAAATCAACAATTGAGAGGTACAAAAGGCATCTGCAGATTCTTCAAC 279  
| | | | |  
QY 286 CCTCCTTCGTCACCGAAGCTAATACTAGTACTATCAGCAAGAACCTCTAAGCTTCGG 345  
| | | | |  
Db 280 ACTGGTCTGTTTCTGAAGCCAATGCTCAGTACTACCAGCAAGAGCTGCCAAGCTGCGT 339  
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QY 346 AGGCAGATTCCAGATATTCAGAAATCAATAGGCATATGTTGGGGAATCACTTGGTTCC 405  
| | | | |  
Db 340 TCCCAAAATGGTAAATTTGAGAAATCAACAGGCATATGCTGGGTGAAGCGCTTAGTTCA 399  
| | | | |  
QY 406 TTGAACCTCAAGGAACCTCAAAACCTTAGAGGAGCTCTTGAAGAAAGGAATCAGCCGTCTC 465  
| | | | |  
Db 400 TTGAGTGTGAAGGAACCTTAAGAGTTTGGAAATACGACTTGAGAAAGGAATGAGCAAT 459  
| | | | |  
QY 466 CGTCCCAAAAGAAATGAGCTGTAGTGGCAGAGATAGACTATATGCAGAAAGGGAATG 525  
| | | | |  
Db 460 CGTTCCAAAAGAAATGAGCTGTGTTGCGAAGAAATCGAGTATATGCAGAAAGGAGGAGTT 519  
| | | | |  
QY 526 GAGTTGCAACACAATAACATGTACTCTCGAGCAAAAGATAGCCGAAGGCCCCAGA 579  
| | | | |  
Db 520 GACTTGCAACAACAATAACAGCTTCTCCGAGCAAAAGATTTCAGAGAAATGAAGA 573  
| | | | |  
RESULT 11

US-09-410-464-10  
; Sequence 10, Application US/09410464  
; Patent No. 6395892  
; GENERAL INFORMATION:  
; APPLICANT: Strauss et al.  
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in  
; FILE REFERENCE: 53375  
; CURRENT APPLICATION NUMBER: US/09/410,464  
; CURRENT FILING DATE: 1999-10-01  
; EARLIER APPLICATION NUMBER: 09/287,700  
; EARLIER FILING DATE: 1999-04-06  
; EARLIER APPLICATION NUMBER: 60/080,851  
; EARLIER FILING DATE: 1998-04-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 1219  
; TYPE: DNA  
; ORGANISM: Populus balsamifera subsp. trichocarpa  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (196)..(921)  
US-09-410-464-10  
  
Query Match 34.1%; Score 305.2; DB 4; Length 1219;  
Best Local Similarity 73.2%; Pred. No. 3.5e-84;  
Matches 391; Conservative 0; Mismatches 143; Indels 0; Gaps 0;  
  
QY 46 AAGAACTAGGAGAGGGGAAATAGAGATAAGAGGATAGAGACACACAAATCGTCAA 105  
Db 235 AGGAAGCTGGGAGGGAAGGTGGAGATCAAGCGGATCGAGAACCCCAATCGCCAA 294  
  
QY 106 GTTACTTCTGCAACGACGCAATGGTCTTCTCAAGAAAGCTTATGAACCTCTCTCTTG 165  
Db 295 GTCACTTCTGCAAAAGGCGGAGTGGTGTCTCAAGAAAGCTTATCTCTCTCT 354  
  
QY 166 TGTGATGCCGAAGTTGCCCTCGTCACTCTTCTCCACTCGTGGCCGCTCTATGAGTACGCC 225  
Db 355 TCGGATGCTGAGTTGCACTCATCGTCTCTCTAGCCGCGCTGCTTATGAGTACTCT 414  
  
QY 226 AACCAAGTGTGAGGGGTACAAATGAAAGGTACAAAGAAAGCTTGTCCGATGCCGTCAC 285  
Db 415 AAGATAGTGTCAAAATCAAAATGAGAGGTACAAAGGATCTCGAGATCTTCAAAAC 474  
  
QY 286 CTTCTTCCGTCACCGAAGCTAATCTCAGTACTATCAGCAAGAAAGCTCTAAGCTTCGG 345  
Db 475 ACTGGGTGTGTTCTGAAGCCAAATGCTCAGTACTACCAAGCAAGAGCTGCCAAGCTGCGT 534  
  
QY 346 AGCAGATTCGAGATATTCAGAAATTCAGAAATAGGCATATTTGGGGAATCACTTGGTTCC 405  
Db 535 TCCCAAAATGGTAATTTGCAGAAATTCAAACAGGCATATGCTGGTGAAGCGCTTAGTTCA 594  
  
QY 406 TTGAACCTCAAGAACTCAAAACCTAGAGGACGCTTGGAAAAGGAATCAGCCGCTGC 465  
Db 595 TTGAGTGTGAAGAACTTAAGAGTTTGGAAATACGACTTGAGAAAGGAATTAAGCAGAAAT 654  
  
QY 466 CGCTCCAAAAAGAAATAGCTGTAGTGGCAGAGATAGATATATGCAAGAGGGAATG 525  
Db 655 CGTTCCAAAAAGAAATAGCTGTGTTGTCAGAAATCAGTATATGCAAGAGGAGGAGTT 714  
  
QY 526 GAGTTGCAACACAATAACATGTACCTGGGAGCAAGATAGCCGAAGCGCCAGA 579  
Db 715 GACTTGCAACAACAATAACAGCTTCTCCGAGCAAGAAATTTAGAGAGATGAAGA 768

RESULT 12  
US-09-433-579-1  
; Sequence 1, Application US/09433579  
; Patent No. 644877  
; GENERAL INFORMATION:  
; APPLICANT: Rottmann, William H.  
; TITLE OF INVENTION: LSAG Gene

FILE REFERENCE: LSAG Gene  
; CURRENT APPLICATION NUMBER: US/09/433,579  
; CURRENT FILING DATE: 1999-11-04  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 1297  
; TYPE: DNA  
; ORGANISM: Liquidambar styraciflua  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (331)..(1008)  
US-09-433-579-1  
  
Query Match 32.1%; Score 287.8; DB 4; Length 1297;  
Best Local Similarity 65.5%; Pred. No. 8.2e-79;  
Matches 462; Conservative 0; Mismatches 222; Indels 21; Gaps 2;  
  
QY 49 AAACCTAGGGAGAGGGAATAATAGAGATAAAGAGGATAGAGAACACAAATCGTCAAGTT 108  
Db 328 AAAATGGGTAGGGGAAAGATCGAGATCAAGCGGATCGAGAACACGACAAACCGCAAGTC 387  
  
QY 109 ACTTCTGCAAAACGACGCAATGGTCTTCTCAAGAAAGCTTATGAACCTCTCTGTCTGTGT 168  
Db 388 ACCTTCTGTAAACGCGCAACGCGCTTACTCAAGAAAGGCTATGAATTAATCTGTCTCTGT 447  
  
QY 169 GATGCCGAAGTTGCCCTCGTCACTCTTCTCCACTCGTGGCGGTCTCTATGAGTACGCCAAC 228  
Db 448 GATGCCGAGTAGCCCTTATCTCTCTACCGTGGCGGCTTACGAGTATGCCAAC 507  
  
QY 229 AACAGTGTGAGGGGTACAATGAAAGGTACAAGAAAGCTTGTCCGATGCCCGTCAACCC 288  
Db 508 AACAGTGTGAAAGCAACAATGAGAGGTATAGAAAGGCACTCTGGGATTCCTCCAATACT 567  
  
QY 289 CCTTCGCTCAGCGAAGCTAATCTCAGTACTATCAGCAAGAAAGCTCTAAGCTTCGGAGG 348  
Db 568 GGATCTGTTTCTGAAGCCCAATGCTCAGTTCTACCAAGAAAGCTGGCAAACTGGGTAAC 627  
  
QY 349 CAGATTCGAGATATTCAGAAATTCAGATAGGCAATATGTTGGGGAATCACTTGGTTCCTTG 408  
Db 628 CAAATCAGGAATATGCAAGATACAAACAGGACTATGCTGGGTGAGTCTTTGGGCTCTCTG 687  
  
QY 409 AACTTCAAGGAACCTCAAAACCTAGAGGAGCTTGTGAAAAGGAATCAGCCGCTCCGC 468  
Db 688 ACTCCCAAGAACTCAAGGGCTGGAGACTAAATTAGAGAAAGGCAATAGCAAAATAAGG 747  
  
QY 469 TCCAAAAGAAATGAGCTGTAGTGGCAGAGATAGATATATGCAAGAGGGAATGGAG 528  
Db 748 TCCAAAAGAAATGAGCTACTGTTTCCGAAATTAATACATGCAAAAGAGGGAATCGAC 807  
  
QY 529 TTGCAACACAATAACATGTACCTGCGAGCAAAAGATAGCCGAAGGCGCCAGATTGAATCCG 588  
Db 808 TTGCACAATGATACCAAGTATCTCCGAGCAAAATAGCTGAACACGAGAGA----- 858  
  
QY 589 GACCAGCAGGAATCGAGTGTGATACAGGGGACGACAGTTTACGAATCCGGTGTATCTTCT 648  
Db 859 GCTCAACAGCAAAATGAACCTTGTATGCGAGGTGGATCAAACTATGAGGTCTTGCCATC- 914  
  
QY 649 CATGACAGTCCGAGCAATTAATTCGGAACATATATCCGGTGAACCTTCTTGAACCGAAT 708  
Db 915 -----ACAGCCATTGACTCTCGGAACCTTTTCCAAAGTAATGCATTGCAACCCAAT 966  
  
QY 709 CAGCAATTCCTCGGCGCAAGACCAACCTCTCTTCAACTTGTGTAA 753  
Db 967 CATCATTAATCTCTCGCCAAAGATCAAAATGGCCCTTCAATTAGTTAA 1011

RESULT 13  
US-08-460-512-3  
; Sequence 3, Application US/08460512  
; Patent No. 5744693  
; GENERAL INFORMATION:  
; APPLICANT: MEYEROWITZ, Elliot M.

APPLICANT: YANOFKY, Martin F.  
APPLICANT: MA, Hong  
TITLE OF INVENTION: PLANTS HAVING ALTERED FLORAL DEVELOPMENT  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Richard F. Trecartin  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/460,512  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/293,278  
FILING DATE:  
APPLICATION NUMBER: US/07/956,694  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-57322/RFT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1097 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 126..884  
US-08-460-512-3

Query Match 31.7%; Score 284.4; DB 1; Length 1097;  
Best Local Similarity 70.3%; Pred. No. 8.4e-78;  
Matches 381; Conservative 0; Mismatches 161; Indels 0; Gaps 0;

Qy 46 AAGAACTAGGAGAGGAGAAATAGAGATAAAGAGATAGAGAACACACAAATCGTCAA 105  
Db 168 AGGAAGCTGGAGAGAGAAATGCTCAAGAAATGCTTCAAGAAAGCTTACGAATCTCTGTTCTT 227  
Qy 106 GTTACTTTCTGCAACGACGCAATGGTCTCTCAAGAAAGCTTATGAATCTCTGTTG 165  
Db 228 GTTACTTTCTGCAACGACGCAATGGTCTCTCAAGAAAGCTTACGAATCTCTGTTCTT 287  
Qy 166 TGTGATGCCGAAGTTCCTGCTGCTATCTTCTCACTCGTGGCGGCTCTATGAGTACGCC 225  
Db 288 TGTGATGCTGAAGTCGCACTATCTTCTCTAGCCGCGGCTCTATGAGTACTCA 347  
Qy 226 AACACAGTGTGAGGGGTACAAATGAAAGGTACAGAAAGCTTGTCCGATGCCGTCAAC 285  
Db 348 AACACAGTGTAAAGGGACAATGAGAGGTACAGAAAGCAATATCGGATAATCTTAAC 407  
Qy 286 CCTCTTCCTGACCGAAGTAAATCTACTACTATCAGAAAGAGCCCTTAAGCTTCGG 345  
Db 408 ACCGGATCCGTGGCAGAAATTAATGCACAGTATTATCAACAAAGATCTGCCAAATTCGCT 467  
Qy 346 AGGCAGATTCGAGATATTCAGAAATCAAAATAGGCATATGTTGGGAATCACTTGGTTCC 405  
Db 468 CAACAAATATCAGCATACAGAACTCGAACAGGCAATGATGGGTGAGAGGATGGGTCA 527  
Qy 406 TTGAACCTTCAAGGAACCTCAAAAACCTTAGAGGACGCTCTTGAAGAAAGGAATCAGCGGTGTC 465

Db 528 ATGTCTCCCAAGAGCTCAGGAACCTTGAAGGCGAGATTAGACAGAAAGTGTATATCGAATC 587  
Qy 466 CGTCCCAAAAGAAATGAGCTGTTAGTGGCAGAGATAGAGTATATGCAGAAAGAGGAAATG 525  
Db 588 CGATCCCAAGAAAGCAACTCTTATTCGCCGAATTGACTACATGCAGAAAGAGAGAACTT 647  
Qy 526 GAGTTGCAACACAATAACATGTACCTGCGAGCAAGATAGCCGAAGGCCCGCAGATTGAAT 585  
Db 648 GATTTCATAACGATAACCAAGCTTCTTCGTGCTAAAGATAGCTGAAAATGAGAGGAACAAT 707  
Qy 586 CC 587  
Db 708 CC 709  
RESULT 14  
US-08-460-512-1  
Sequence 1, Application US/08460512  
Patent No. 5744693  
GENERAL INFORMATION:  
APPLICANT: MEYEROWITZ, Elliot M.  
APPLICANT: YANOFKY, Martin F.  
APPLICANT: MA, Hong  
TITLE OF INVENTION: PLANTS HAVING ALTERED FLORAL DEVELOPMENT  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Richard F. Trecartin  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/460,512  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/293,278  
FILING DATE:  
APPLICATION NUMBER: US/07/956,694  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-57322/RFT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1457 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 416..1270  
US-08-460-512-1

Query Match 30.8%; Score 275.8; DB 1; Length 1457;  
Best Local Similarity 69.2%; Pred. No. 4.3e-75;  
Matches 376; Conservative 0; Mismatches 167; Indels 0; Gaps 0;

Qy 46 AAGAACTAGGAGAGGAGAAATAGAGATAAAGAGATAGAGAACACACAAATCGTCAA 105  
Db 557 AGGAATCTGGAGAGAGAAAGATCGAAATCAAAACGATCGAGAACACAGAAATCGTCAA 616

QY 106 GTTACTTCTGCAAGACCAATGGTCTCTCAAGAAAGCTTATGAACCTCTCTGTCTTG 165  
Db 617 GTCACITTTTGCACACGCTAGAAATGGTTTCTCAAGAAAGCTTACGAGCTCTCTGTCTC 676  
QY 166 TGTGATGCCGAAGTTGCCCTGCTATCTTCTCCACTCGTGGCCGTCTCTATGATGACGCC 225  
Db 677 TGTGATGCTGAAGTGCACATCATCTTTCTCTACCCGCTGCTCTCTATGATGATCTCT 736  
QY 226 AACACAGTGTGAGGGGTACAATTTGAAAGGTACAAAGAAAGCTTGTCCGATGCCGTCAAC 285  
Db 737 AACACAGTGTAAAAGGTACTATTGAGAGGTACAAAGCAATATCGGACAATCTTAAC 796  
QY 286 CTTCTTCCGTCACCGAAGCTAATACTCACTACTATCAGCAAGAGCCCTTAAGCTTCGG 345  
Db 797 ACCGGATCGGTGGCAGAAATTAATGCACAGTATTATCAACAAGAAATCAGCCAAATTCGCT 856  
QY 346 AGGCAGATTCGAGATATTCAAAATTCAGATAGGCATATTGTTGGGAATCATTGGTTCC 405  
Db 857 CAACAATTTATCAGCATACAAACCTCAACAGGCAATTGATGGTGAGAGGATAGGGTCA 916  
QY 406 TTGAACCTTCAAGGAACCTCAAAAACCTAGAGGACCTCTTGAAGAAAGGATCAGCCGTGC 465  
Db 917 ATGTTCCCAAGAGCTCAGGAACCTTGGAGGCAGATTAGAGAGAGTATTACCCGAATC 976  
QY 466 CGCTCCAAAAGAAATGAGCTCTTAGTGGCAGAGATAGATATATGCAGAGAGGGAATG 525  
Db 977 CGATCCAAAGAAATGAGCTCTTATTTCTGAAATCGGACTACATCGAGAAAAGAAAGTT 1036  
QY 526 GAGTTGCAACAAATACATGTACCTGCGAGCAAGATAGCCGAGGCGCCAGATTGAAT 585  
Db 1037 GATTGCAATAACGATAACCAAGATTCTTCTGTCAAAGATAGCTGAAATAGAGGAAACAT 1096  
QY 586 CCG 588  
Db 1097 CCG 1099

RESULT 15  
US-09-067-800-4  
; Sequence 4, Application US/09067800  
; Patent No. 6198024  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin F.  
; APPLICANT: Ferrandiz, Cristina  
; TITLE OF INVENTION: Seed Plants Characterized by Delayed  
; TITLE OF INVENTION: Seed Dispersal  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/067,800  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UD 2948  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 6138 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 1..6138  
; OTHER INFORMATION: /label= AGL5\_promoter  
; OTHER INFORMATION: /note= "Nucleotide sequence of the AGL5 promoter."  
US-09-067-800-4  
Query Match 21.0%; Score 188; DB 4; Length 6138;  
Best Local Similarity 89.0%; Pred. No. 8.7e-48;  
Matches 203; Conservative 0; Mismatches 25; Indels 0; Gaps 0;  
QY 6 AATGGAGGAGGTGGGAGTAGTCACGACCCAGAGAGTAGCAAGAACTAGGGAGAGGGAA 65  
Db 2700 AATGGAGGAGGTGGGAGTAGTAATGAAGTAGCAGAGAGCAGCAAGAAAGATAGGGAGAGGGAA 2759  
QY 66 AATAGAGATAAAGAGGATAGAGAAACACAAATCGTCAAGTTACTTTCTGCAAAACGAGG 125  
Db 2760 GATAGAGATAAAGAGGATAGAGAAACACTAGCAATCGTCAAGTCACTTTCTGCAAAACGAGG 2819  
QY 126 CAATGGTCTTCTCAAGAAAGCTTATGAACCTCTCTCTTGTGTGATGCCGAAAGTTGCCCT 185  
Db 2820 CAATGGTCTTCTCAAGAAAGCTTATGAGCTCTCTCTTGTGTGACGCTCAGGTTGCTCT 2879  
QY 186 CGTCATCTTCTCCACTCGTGGCCGTCCTCTATGATGATGACGCAACACAG 233  
Db 2880 TGTCTCTTCTCCACTCGAGGCCGTCCTACGAGTACGCCCAACACAG 2927  
Search completed: February 2, 2003, 08:20:47  
Job time : 70.9887 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 2, 2003, 08:21:19 ; Search time 1623.91 Seconds  
(without alignments)  
8935.939 Million cell updates/sec

Title: US-09-978-382A-3

Perfect score: 896

Sequence: 1 ggatcaatggaggaaggtgg.....actgtgttcttctgttca 896

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_estl:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pln:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fun:\*

23: em\_gss\_mam:\*

24: em\_gss\_mus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description        |
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| 2          | 315.4 | 35.2        | 686    | BQ411600 | BQ411600 GA_Ed004  |
| 3          | 313.8 | 35.0        | 656    | BQ411583 | BQ411583 GA_Ed004  |
| 4          | 312.4 | 34.9        | 748    | BI311095 | BI311095 EST531284 |
| 5          | 311.6 | 34.8        | 624    | AW277843 | AW277843 sf87d01.y |
| 6          | 306.4 | 34.2        | 754    | BI310910 | BI310910 EST531266 |

|    |       |      |     |    |          |                    |
|----|-------|------|-----|----|----------|--------------------|
| 7  | 302.4 | 33.8 | 636 | 14 | BQ123247 | BQ123247 EST608823 |
| 8  | 299.8 | 33.5 | 656 | 10 | BE659918 | BE659918 1299 Gmax |
| 9  | 299   | 33.4 | 548 | 10 | AW277299 | AW277299 sf80e05.y |
| 10 | 295.8 | 33.0 | 548 | 10 | BE434089 | BE434089 EST405167 |
| 11 | 292.2 | 32.6 | 555 | 13 | BI272847 | BI272847 NF097G09F |
| 12 | 290.6 | 32.4 | 538 | 10 | BE433121 | BE433121 EST399650 |
| 13 | 288   | 32.1 | 776 | 12 | BG445079 | BG445079 GA_Ea002  |
| 14 | 288   | 32.1 | 866 | 12 | BG441292 | BG441292 GA_Ea001  |
| 15 | 288   | 32.1 | 892 | 12 | BG444639 | BG444639 GA_Ea002  |
| 16 | 286   | 31.9 | 597 | 9  | AI729115 | AI729115 BNLGH1126 |
| 17 | 285.8 | 31.9 | 642 | 9  | AI725968 | AI725968 BNLGH1137 |
| 18 | 281.4 | 31.4 | 802 | 13 | BI925669 | BI925669 EST545558 |
| 19 | 280.2 | 31.3 | 960 | 12 | BG445265 | BG445265 GA_Ea002  |
| 20 | 278.6 | 31.1 | 754 | 9  | AI731375 | AI731375 BNLGH1938 |
| 21 | 277.2 | 30.9 | 761 | 9  | AI731368 | AI731368 BNLGH1937 |
| 22 | 276.4 | 30.8 | 632 | 10 | AW185524 | AW185524 se80h09.y |
| 23 | 275.6 | 30.8 | 848 | 12 | BG445047 | BG445047 GA_Ea002  |
| 24 | 274   | 30.6 | 649 | 10 | AW184799 | AW184799 se82f12.y |
| 25 | 273.4 | 30.5 | 929 | 12 | BG444491 | BG444491 GA_Ea002  |
| 26 | 272.8 | 30.4 | 562 | 9  | AI727662 | AI727662 BNLGH1854 |
| 27 | 271.8 | 30.3 | 607 | 10 | AW705451 | AW705451 sk49c05.y |
| 28 | 271.6 | 30.3 | 885 | 14 | BQ796770 | BQ796770 EST 5708  |
| 29 | 269.8 | 30.1 | 539 | 9  | AI771796 | AI771796 EST252896 |
| 30 | 267.2 | 29.8 | 811 | 17 | AQ250561 | AQ250561 T12C11-Sp |
| 31 | 266.4 | 29.7 | 498 | 12 | BF112843 | BF112843 EST440433 |
| 32 | 265.2 | 29.6 | 537 | 9  | AI486290 | AI486290 EST244611 |
| 33 | 262.8 | 29.3 | 608 | 10 | AW278878 | AW278878 sf99h09.y |
| 34 | 262   | 29.2 | 615 | 10 | AV557878 | AV557878 AV557878  |
| 35 | 261   | 29.1 | 698 | 10 | BE659915 | BE659915 7-HA Gmax |
| 36 | 260.4 | 29.1 | 586 | 12 | BG446848 | BG446848 GA_Eb003  |
| 37 | 260   | 29.0 | 597 | 10 | AW704750 | AW704750 sk55a06.y |
| 38 | 258.2 | 28.8 | 566 | 9  | AI728519 | AI728519 BNLGH1109 |
| 39 | 257.2 | 28.7 | 618 | 9  | AI484747 | AI484747 EST243008 |
| 40 | 255.2 | 28.5 | 754 | 13 | BI311053 | BI311053 EST531280 |
| 41 | 251.4 | 28.1 | 613 | 10 | BE659913 | BE659913 3-D9 Gmax |
| 42 | 249.8 | 27.9 | 550 | 10 | BE494811 | BE494811 WHE1273_H |
| 43 | 249.4 | 27.8 | 468 | 10 | BE431937 | BE431937 EST398466 |
| 44 | 245.8 | 27.4 | 584 | 12 | BG442607 | BG442607 GA_Ea001  |
| 45 | 243.8 | 27.2 | 700 | 9  | AL509053 | AL509053 AL509053  |

#### ALIGNMENTS

RESULT 1  
BI933168

LOCUS

DEFINITION

ACCESION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BI933168 715 bp mRNA linear EST 18-OCT-2001  
EST553057 tomato flower, 8 mm to preanthesis buds Lycopersicon  
esculentum cDNA clone cT0C25K8 5' end, mRNA sequence.

BI933168  
BI933168.1 GI:16247640

EST.

tomato.

Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum;

Lycopersicon.

1 (bases 1 to 715)

van der Hoeven,R.S., Bezzerides,J.L., Karamycheva,S.A., Tsai,J.,

Utterback,T., Van Aken,S., Ronning,C.M., Nierman,W., Fraser,C.M.,

Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.

Generation of ESTs from tomato flower tissue, buds 8 mm -

preanthesis

Unpublished (2001)

Contact: CUGI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>

This clone is available through the Clemson University Genomics

Institute

Seq primer: T3.

```
FEATURES
source
Location/Qualifiers
1..715
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cTOC25K8"
/clone_lib="tomato flower, 8 mm to preanthesis buds"
/tissue_type="flower"
/dev_stage="buds 8mm to preanthesis"
/notes="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: Cornell University; sequencing: The
Institute for Genomic Research; Flower buds and flowers
were taken from greenhouse plants (4-8 wks old, TA496).
They were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."

BASE COUNT      251 a   131 c   167 g   166 t
ORIGIN
Query Match      35.7%; Score 319.8; DB 13; Length 715;
Best Local Similarity 72.0%; Pred. No. 4.8e-73;
Matches 417; Conservative 0; Mismatches 162; Indels 0; Gaps 0;

QY 46 AAGAACTAGGAGAGGGAAAATAGAGATAAGAGGATAGAGAACACACAAATCGTCAA 105
Db 108 AGGAACTAGGAAGGGGAAAATGAGATCAAAAGGATCGAAACAGGACGATCGACAA 167
QY 106 GTTACTTTCTGCAAAACGACGCAATGGTCTTCTCAAGAAAGCTTATGAACCTCTGTGCTTG 165
Db 168 GTAACATTCTGCAAGAGCGCAATGGTTGCTTAAAGGCTTATGAATTGCTGTGCTC 227
QY 166 TGTGATGCGGAAGTTGCCCTCGTCATCTTCCACTCGTGGCGCTCTCTATGATAGGCC 225
Db 228 TGTGATGCTGAGGTGCTTGGTTGCTTCTCAACAGAGGACGACTCTATGATATGCC 287
QY 226 AACAACTGTGAGGGGTACAATTGAAGGTACAAGAAAGCTTGTTCGATGCCGTCAAC 285
Db 288 AACAACTGTGAAGCAACAATCGAGAGGTACAAGAAAGCATGCTCAGATTCTCTCAAC 347
QY 286 CCTCCTTCGTCACCGAAGCTAATACAGTACTATCAGCAAGAAGCTCTAAGCTTCGG 345
Db 348 ACTGGTTCAGTATCCGAGGCCAATGCTCAGTATTACGACAGAAGCTCTCCAACTCGC 407
QY 346 AGGCAGATTTCGAGATATTCAGAAATTCAGAAATTTGTTGGGGAATCACTTGGTTCC 405
Db 408 GCACAAATTTGAAATCTGATGAACCAACAGGAACATGATGGGTGAAGCTTTGTCTGGA 467
QY 406 TTGAACTTCAAGGAACCTCAAAACCTAGAAGGACGCTTTGAAAAAGGAATCAGCCGTGC 465
Db 468 ATGAAACTCAAGAACTGAAGATCTGGAGCAAAAGAAATTTGAAAAGGGGATTAGCAAAATC 527
QY 466 CGCTCCAAAAGAAATGAGCTGTTAGTGGCAGAGATAGATATATGCAGAAGGGAATG 525
Db 528 CGATCCAAAAGAAATGAGCTGTTGTTGCTGAAATTTGAGTATATGCAGAAGGGAAGTT 587
QY 526 GAGTTGCAACACAATAACATGTACCTGCGAGCAAAAGATAGCCGAAGGCCAGATTGAAT 585
Db 588 GATTACACAACAACAATCAGTACCTGAGAGCCAAAGATTGCTGAAACTGAGAGAGCTCAG 647
QY 586 CCGGACCAAGAGGAATCGAGTGTGATACAAGGGACGACA 624
Db 648 CATCAGCATCAGCAGATGAACCTTGATGCCAGGGAGGTCA 686

RESULT 2
BO411600
LOCUS
DEFINITION
BO411600
BO411600
BO411600.1 GI:21099287
KEYWORDS
EST.
SOURCE
Gossypium arboreum.
ORGANISM
Gossypium arboreum
```

```
REFERENCE
AUTHORS
Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry
D., Wood,T.C., Leslie,A. and Wilkins,T.A.
TITLE
An integrated analysis of the genetics, development, and evolution
of the cotton fiber
JOURNAL
unpublished (2000)
COMMENT
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total High Quality bases = 612
Seq primer: TAATACGACTCACTATAGGG
High quality sequence start: 2
High quality sequence stop: 685.
FEATURES
Location/Qualifiers
1..686
/organism="Gossypium arboreum"
/strain="AKA"
/cultivar="8400"
/db_xref="taxon:29729"
/clone="GA_Ed0041B08f"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
dpa"
/lab_host="E. coli"
/notes="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT      236 a   153 c   151 g   146 t
ORIGIN
Query Match      35.2%; Score 315.4; DB 14; Length 686;
Best Local Similarity 73.9%; Pred. No. 6.7e-72;
Matches 400; Conservative 0; Mismatches 141; Indels 0; Gaps 0;

QY 46 AAGAACTAGGAGAGGGAAAATAGAGATAAGAGGATAGAGAACACACAAATCGTCAA 105
Db 57 AAAAAATGGAGAGGCAAAATCGAGATTAAAGGATCGAGAACACCCTAATCGACAA 116
QY 106 GTTACTTTCTGCAAAACGACGCAATGGTCTTCTCAAGAAAGCTTATGAACCTCTGTGCTTG 165
Db 117 GTTACCTTCTGCAAGCGCCCAATGGACTGCTCAAAAGGCTATGAATTATCTGTTCTT 176
QY 166 TGTGATGCCGAAGTTGCCCTCGTCATCTTCTCCACTCGTGGCGCTCTCTATGATAGTCCG 225
Db 177 TGTGATGCTGAGGTGGCTCTCATAGTCTTCTCCAGCGTGGCCGCTCTATGAAATATGCT 236
QY 226 AACAACTGTGAGGGGTACAATTGAAGGTACAAGAAAGCTTGTTCGATGCCGTCAAC 285
Db 237 AACAACTGTGAGAGCAACAATTTGAGAGATACAAGAAAGCATGCTCAGATGCAACAACT 296
QY 286 CCTCCTTCGTCACCGAAGCTAATACCTCAGTACTATCAGCAAGAAGCTCTAAGCTTCGG 345
Db 297 CCAGGGTCTGTGGCTGAAGCCATTATTCAGTCTACCAAGCAAGCAACCAAACTCCGA 356
QY 346 AGGCAGATTTCGAGATATTCAGAAATTCAAATAGGCATATTTGTTGGGAATCACTTGGTTCC 405
Db 357 CGACAAATTCGTGATGTTTCAGAACATGAACAGCATATCTTGGAGAGGCTCTGAGTCA 416
QY 406 TTCAACTTCAGGAACCTCAAAACCTAGAGGACGCTTGTGAAAAAGGAATCAGCCGTGTC 465
Db 417 TTGACCTTTAAGGAACCTCAAGAACCTTGAAGGAGGCTGAGAAAGGCATTGTAGAACT 476
QY 466 CGTCCAAAAAGAAATGAGCTGTTAGTGGCAGAGATAGAGTATATGCAGAAGAGGGAATG 525
Db 477 AGATCCAAAAAGAAACGAATTACTGTTTGCAGAAATTTGGATTTCATGCAAAAAGAGGAAGTT 536
QY 526 GAGTTGCAACACAATAACATGTACCTGCGAGCAAAAGATAGCCGAAGGCCAGATTGAAT 585
```

[illegible]



Gigapack III Gold packaging extracts. Plasmids containing  
cDNA inserts were excised from the recombinant lambda-Zap  
phage using Ex-assist helper phage and propagated in  
XL0LR cells."

|                       |                                                                     |                                                               |                 |             |                 |
|-----------------------|---------------------------------------------------------------------|---------------------------------------------------------------|-----------------|-------------|-----------------|
| BASE COUNT            | 258 a                                                               | 136 c                                                         | 161 g           | 193 t       |                 |
| ORIGIN                |                                                                     |                                                               |                 |             |                 |
| Query Match           | 34.9%;                                                              | Score 312.4;                                                  | DB 13;          | Length 748; |                 |
| Best Local Similarity | 69.2%;                                                              | Pred. No. 4.2e-71;                                            |                 |             |                 |
| Matches 462;          | Conservative                                                        | 0;                                                            | Mismatches 191; | Indels 15;  | Gaps 2;         |
| QY                    | 46                                                                  | AAGAACTAGGAGAGGAAATAGAGATAAGAGGATAGAGACACACAAATCGTCAA         | 105             |             |                 |
| Db                    | 83                                                                  | AAGAAATGGAAGAGGAAATTAATCAAGAGGATTGAACACACTACCAATAGGCAA        | 142             |             |                 |
| QY                    | 106                                                                 | GTTACTTTCTCAACGACGCAATGGTCTTCTCAAGAAAGCTTATGAACCTCTCTGCTTG    | 165             |             |                 |
| Db                    | 143                                                                 | GTCACATTTTCCAAAGCAGCAATGGATTGTTGAGAAAGCTTATGAATATCCGTTCTT     | 202             |             |                 |
| QY                    | 166                                                                 | TGTGATGCCGAAGTTCCTCGTCTATCTTCCACTCGTGGCCGCTCTCTATGATGACGCC    | 225             |             |                 |
| Db                    | 203                                                                 | TGTGATGCCGAAGTTCCTCGTCTATCTTCCACTCGCGGTCGTTTGTATGATGATGCC     | 262             |             |                 |
| QY                    | 226                                                                 | AACAACAGTCTGAGGGGTACATATTGAAGGTACAGAAAGCTTGTCCGATGCCGTCAAC    | 285             |             |                 |
| Db                    | 263                                                                 | AACAACAGTGTAGACCAACTATTGAAGGTACAAAAAGCATGTGCTGCTTCCACTAAC     | 322             |             |                 |
| QY                    | 286                                                                 | CTCTCTTCGTCACCGAAGCTAATACTCAGTACTATCAGCAAGAGCCCTTAAGTTCGG     | 345             |             |                 |
| Db                    | 323                                                                 | GCAGAACTGTATCTGAAGCTAATACCCAGTTTACAGCAAGAATCATCCAAATTGAGA     | 382             |             |                 |
| QY                    | 346                                                                 | AGCGATATTCAGATATTCAGAAATTCAGATATAGGCATATTTGTTGGGAATCAGTTGTTCC | 405             |             |                 |
| Db                    | 383                                                                 | ACACAGATTCGAGATATTCAGAAATTCAGATATAGCACATCCTTGGTGAAGCTTAGGATCT | 442             |             |                 |
| QY                    | 406                                                                 | TGAACCTCAAGGAAGTCAAAAACTAGAGGACGCTTGTGAAAAAGGAATCAGCCGTGC     | 465             |             |                 |
| Db                    | 443                                                                 | CTAAGTCTCAAGAACTGAAGAACTCTGAGGTAGATTGGAGAAAGTTTAAGCAGAGTT     | 502             |             |                 |
| QY                    | 466                                                                 | CGCTCCAAAAAGAAATGAGCTGTAGTGGCAGAGATAGATATATGAGAGAGGAGGAAATG   | 525             |             |                 |
| Db                    | 503                                                                 | AGATCTAGAAAGCATGAGACTTGTGTTGCTGATGTGGAGTTCATGCAAAAGCGGAAAT    | 562             |             |                 |
| QY                    | 526                                                                 | GAGTTGCAACAAATACATGATGACCTCGAGCAAGATAGCGGAGCGCCAGATTTGAAT     | 585             |             |                 |
| Db                    | 563                                                                 | GAGCTGCAAAACCATACAAATATCTACGGGCTAAGATAGCGGAACATGAGAGA-----    | 616             |             |                 |
| QY                    | 586                                                                 | CGGACACGAGGAATCGAGTGTGATACAGGACGACAGTTTACCAATCCGGTGTATCT      | 645             |             |                 |
| Db                    | 617                                                                 | GCTCAACAACGACACATAATTGATGCCAGATCAAAACAATGTGTGATCAGTCTTACCT    | 676             |             |                 |
| QY                    | 646                                                                 | TCTCATGACCAAGTCGACGATTTATAATCGGAATATATTCGGTGTGAACCTTCTTGAAACG | 705             |             |                 |
| Db                    | 677                                                                 | TC-----ATCACAGCATATGACCGGAATTTCTTCCGGTAAATCTTCTTGGATCA        | 727             |             |                 |
| QY                    | 706                                                                 | AATCAGCA                                                      | 713             |             |                 |
| Db                    | 728                                                                 | GATCAGCA                                                      | 735             |             |                 |
| RESULT 5              |                                                                     |                                                               |                 |             |                 |
| AW277843              |                                                                     |                                                               |                 |             |                 |
| LOCUS                 | AW277843                                                            | 624 bp                                                        | mRNA            | linear      | EST 02-DEC-2001 |
| DEFINITION            | sf87d01.y1 Gm-cl019 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: |                                                               |                 |             |                 |
|                       | Gm-cl019-3098 5' similar to SW:AGL5_ARATH P29385 FLORAL HOMEOTIC    |                                                               |                 |             |                 |
|                       | PROTEIN AGL5. ; mRNA sequence.                                      |                                                               |                 |             |                 |
| ACCESSION             | AW277843                                                            |                                                               |                 |             |                 |
| VERSION               | AW277843.1                                                          | GI:6666384                                                    |                 |             |                 |
| KEYWORDS              | EST.                                                                |                                                               |                 |             |                 |
| SOURCE                | soybean.                                                            |                                                               |                 |             |                 |
|                       | Glycine max                                                         |                                                               |                 |             |                 |
| ORGANISM              | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  |                                                               |                 |             |                 |
|                       | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;        |                                                               |                 |             |                 |

Residae; eurousids I; Fabaales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.  
1 (bases 1 to 624)  
Shoemaker,R., Kelm,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna  
A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,  
Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers  
Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk  
R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann  
R., Waterston,R. and Wilson,R.  
Public Soybean EST Project  
Unpublished (1999)  
Contact: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest park parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available through: ResGen, Invitrogen Corp. 2130  
South Memorial Parkway Huntsville, AL 35801 For further information  
call: (800)-533-4363 or contact via email: ccu@resgen.com  
Insert Length: 1024 Std Error: 0.00  
Seq primer: -40RP from Gibco  
High quality sequence stop: 446.

FEATURES  
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1. .624  
/organism="Glycine max"  
/db\_xref="taxon:3847"  
/clone="GENOME SYSTEMS CLONE ID: Gm-cl019-3098"  
/clone\_lib="Gm-cl019"  
/tissue\_type="immature seed coats of greenhouse grown  
plants"  
/lab\_host="DH10B (gibco BRL)"  
/note="Vector: pSPORT1 (Life Technologies); Site\_1: Not I;  
Site\_2: Sal I; This cDNA library was constructed from mrna  
isolated from immature seed coats (200-300 mgs) of  
greenhouse grown plants. The library was prepared using  
the Life Technologies pSuperScript cDNA library  
construction kit. Complementary DNA was synthesized from  
mrna using a poly (dT) sequence with a Not I restriction  
site. Sal I linker adapters were ligated to the  
blunt-ended cDNA fragments followed by Not I digestion.  
The cDNA fragments were directionally cloned into the Not  
I-Sal I restriction site of the pSPORT1 vector. The  
ligated cDNA fragments were transformed into E.coli  
ElectroMax DH10B host cells (Gibco BRL). This library was  
constructed by Dr. Lila Vodkin and Dr. Anu Khanna."  
BASE COUNT 210 a 124 c 145 g 142 t 3 others  
ORIGIN

Query Match 34.8%; Score 311.6; DB 10; Length 624;  
Best Local Similarity 71.1%; Pred. No. 6.6e-71;  
Matches 410; Conservative 0; Mismatches 167; Indels 0; Gaps 0;  
QY 3 ATCAATGGAGGAGGTGGGAGTAGTTCACGACGACAGAGATAGCAAGAACTAGGGAGAGG 62  
Db 24 AACCATGGAGGATCCAAATCAAGCTCCAGAGCGTCTTCTCAGAGAAATGGGAAGAGG 83  
QY 63 GAAATAGAGATAAAGAGGATAGAGAACACACAAATCGTCAAGTACTTCTGCAACG 122  
Db 84 GAAGATGAATCAACGGGATCGAGAACACCACCAATAGGCAAGTCACCTTCTGCAAGCG 143  
QY 123 ACGCAATGCTTCTCAAGAAAGCTTATGAACCTCTGTCTGTGTGTGATGCCGAGATTGC 182  
Db 144 CGCAACGGTTGCTGAAAAAGCTTATGAATATCAGTTCTGTGTGATGCTGAAGTTGC 203  
QY 183 CCTCGTCATCTTCTCCACTCGTGGCGTCTCTATGATGATACGCCAACACAGTGTGAGGGG 242  
Db 204 CTTGTTGCTTCTCAACCCCGTGGCGGTTTGTATGAGTATGCCAACACAGTGTAGGGC 263  
QY 243 TACAATGAAGGTACAGAAAGCTTGTTCGATCGCGTCCGCTCCCTTCCGTACCCGA 302  
Db 264 CACTATTGAGAGGTACAAGAGGCAATGCTGCTTCAAAACGACAGATCCGTATCTGA 323

| QY         | 303                                                                                                                                                                                                                                             | AGCTAATACTACTACTATCAGCAAGAAGCCCTCTAAGCTTCGGAGGCAGATTCGAGATAT     | 362             |
|------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------|-----------------|
| Db         | 324                                                                                                                                                                                                                                             | AGTTAACACACAGTTTACCAGCAAGAGTCATCCAAATTGAGAAGACAAATTCGAGATAT      | 383             |
| QY         | 363                                                                                                                                                                                                                                             | TCAGAATTCAAATAGGCATATTTCTGGGGAATCACCTTGGTTCTTGAACCTTCAAGGAAC     | 422             |
| Db         | 384                                                                                                                                                                                                                                             | TCAGAATCTAAACAGGCACATCCTTTGGTGAAGCACCTTGGTTCTCTGAGTCTCAAGGAAC    | 443             |
| QY         | 423                                                                                                                                                                                                                                             | CRAAAACCTAGAAGGACGCTTTGAAAAGGAATCAGCGTGTCCGCTCCAAAAGAAATCA       | 482             |
| Db         | 444                                                                                                                                                                                                                                             | AAAGAACCCTCGAGGTAGATTGCGAAGAGGATTAAGCAGAGTTAGATCTAGAAGCATGA      | 503             |
| QY         | 483                                                                                                                                                                                                                                             | GCTGTTAGTGGCAGAGATAGATATATGCAGAAGAGGGAAATGGAGTTGCAACACAATAA      | 542             |
| Db         | 504                                                                                                                                                                                                                                             | NACATTGTTTGTGTGATGTGGAGTTTCATGCANAAAGCGGAAATTGAGTGTGCANAACCA     | 563             |
| QY         | 543                                                                                                                                                                                                                                             | CATGTACCTCGCAGCAAGATAGATGATATATGCAGAAGAGGGAAATGGAGTTGCAACACAATAA | 579             |
| Db         | 564                                                                                                                                                                                                                                             | CAATTATCTGCGAGCTAAGATAGCTGAACATGAGAGA                            | 600             |
| RESULT 6   |                                                                                                                                                                                                                                                 |                                                                  |                 |
| BI310910   |                                                                                                                                                                                                                                                 |                                                                  |                 |
| LOCUS      | BI310910                                                                                                                                                                                                                                        | 754 bp                                                           | linear          |
| DEFINITION | EST312660 GSD Medicago truncatula cDNA clone pGESD9K22 5' end,                                                                                                                                                                                  |                                                                  | EST 20-JUL-2001 |
| ACCESSION  | BI310910                                                                                                                                                                                                                                        |                                                                  |                 |
| VERSION    | BI310910.1                                                                                                                                                                                                                                      | GI:14985237                                                      |                 |
| KEYWORDS   | EST.                                                                                                                                                                                                                                            |                                                                  |                 |
| SOURCE     | barrel medic.                                                                                                                                                                                                                                   |                                                                  |                 |
| ORGANISM   | Medicago truncatula                                                                                                                                                                                                                             |                                                                  |                 |
|            | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids 1; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.                                   |                                                                  |                 |
| REFERENCE  | 1 (bases 1 to 754)                                                                                                                                                                                                                              |                                                                  |                 |
| AUTHORS    | Grusak, M.A., Samac, D.A., Town, C.D., Van Aken, S., Utterback, T., Cho, J., and Fraser, C.M.                                                                                                                                                   |                                                                  |                 |
| TITLE      | ESTs from developing reproductive tissues of Medicago truncatula                                                                                                                                                                                |                                                                  |                 |
| JOURNAL    | Unpublished (2001)                                                                                                                                                                                                                              |                                                                  |                 |
| COMMENT    | Contact: Michael A. Grusak<br>USDA/ARS Children's Nutrition Research Center<br>Baylor College of Medicine<br>1100 Bates Street, Houston, TX 77030-2600, USA<br>Tel: 713-798-7044<br>Fax: 713-798-7078<br>Email: mgrusak@bcm.tmc.edu<br>B397765e |                                                                  |                 |



Db 164 CGCCGCAACGGTTTCTGCTGAAAAAGCTTATGAATTATCAGTTCTGTGTGATGCTGAAGTT 223

QY 181 GCCTCGTCATCTTCTCCACTCGTGGCGTCTCTATGAGTACGCCAACACACAGTGTGAGG 240

Db 224 GCCTTGTGTCTTCTCAACCGTGGCGTTTGTATGAGTATGCCAACACAGTGTAGG 283

QY 241 GGTACAATTGAAAGGTACAAGAACTTGTTCGGATGCCGTCAACCCCTTCCGTCACC 300

Db 284 GCCACTATTGAGAGGTACAAGAGGCAATGCTGCTCTCAACGCGAGAATCCGTATCT 343

QY 301 GRAGCTAATCTAGTACTATCAGCAAGAAGCTCTAAGCTTCGGAGCGAGATTCGAGAT 360

Db 344 GAAGCTAACACACAGTTTACCAGCAGAGTCATCCAAATTTGAGAAGACAAATTCGAGAT 403

QY 361 ATTCAGAAATTCAAATAGGCATATTTGTTGGGGAATCACTTGGTTCTTGAACCTCAAGGAA 420

Db 404 ATTCAGAAATTCAAACAGGCACATCTTGGTGAAGCATTGGTTCTCTGAGTCTCAAGGAA 463

QY 421 CTCAAAAACCTAGAGGACGCTTGTGAAAAAGGAATCAGCCGTGTCCTCCGCTCCAAAAAGAA 480

Db 464 CTAAGAACCTCGAGGCTAGATTGGAGAAAGGATTAAAGCAGAGTTAGATCTAGAAAGCAT 523

QY 481 GAGCTGTAGTGGCAGAGATAGATATATGAGAGAGGGGAATGAGATTGCAACACAAT 540

Db 524 GAAACATTTGTTGCTGTGATGTGGAGTTTCATGCAAAAGCGGGAATTTGAGCTGCAAAACCA 583

QY 541 AA-CATGTACCTCGAGCAAGATAGCCGAAGGCGCCAGA 579

Db 584 AACCATTATCTCGAGCTAAGATAGCTGAACATGAGAGA 623

RESULT 9

AW277299

LOCUS

DEFINITION

sf80e05.y1 Gm-cl019 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-cl019-2457 5' similar to SW:AGL5\_ARATH\_P29385 FLORAL HOMEOBOX PROTEIN AGL5. ;, mRNA sequence.

AW277299

AW277299.1 GI:6665849

EST.

soybean.

Glycine max

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE

1 (bases 1 to 548)

Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann ,R., Waterston,R. and Willson,R.

Public Soybean EST Project

Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com

Insert length: 949 Std Error: 0.00

Seq primer: -40RP from Gibco

High quality sequence stop: 438.

Location/Qualifiers

1. 548

/organism="Glycine max"

/db\_xref="taxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-cl019-2457"

FEATURES

Source

/clone\_lib="Gm-cl019"

/tissue\_type="Immature seed coats of greenhouse grown plants"

/lab\_host="DH10B (Gibco BRL)"

/note="Vector: pSPORT1 (Life Technologies); Site\_1: Not I; Site\_2: Sal I; This cDNA library was constructed from mRNA isolated from immature seed coats (200-300 mgs) of greenhouse grown plants. The library was prepared using the Life Technologies pSuperScript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly (dT) sequence with a Not I restriction site. Sal I linker adapters were ligated to the blunt-ended cDNA fragments followed by Not I digestion. The cDNA fragments were directionally cloned into the Not I-Sal I restriction site of the pSPORT1 vector. The ligated cDNA fragments were transformed into E.coli ElectroMax DH10B host cells (Gibco BRL). This library was constructed by Dr. Lila Vodkin and Dr. Anu Khanna."

BASE COUNT 187 a 107 c 128 g 126 t

ORIGIN

Query Match 33.4%; Score 299; DB 10; Length 548;

Best Local Similarity 73.8%; Pred. No. 1.3e-67;

Matches 380; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

QY 56 GGAGAGGGAAAAATAGAGATAAAGAGGATAGAGACACACAAATCGTCAAGTTACTTTCT 115

Db 1 GAAGAGGGAAAGATTGAATCAAAACGGATCGAGACACCACCAATAGGCAAGTCACCTTCT 60

QY 116 GCAACGACGCAATGGTCTTCTCAAGAAAGCTTATGAACCTCTCTGTTGTGTGATCGCG 175

Db 61 GCAAGCGCGCAACGGTTTCTGAAAAAGCTTATGAATATATCAGTTCTCTGTGTGATCGT 120

QY 176 AAGTTGCCCTCGTCATCTTCTCCACTCGTGGCGCTCTCTATGAGTACGCCAACACAGTG 235

Db 121 AAGTTGCCCTTGTCTCTTCAACCCGCTGGCGGTTGTATGATGATGCCAACACAGTG 180

QY 236 TGAGGGGTACAATTTGAAAGGTACAGAAAGCTTGTTCGGATGCCGTCAACCCCTCCTTCCG 295

Db 181 TTAGGGCCACTATTGAGAGGTACAGAGGCAAGGCAATGCTGCTTCAAGCGCAGAAATCCG 240

QY 296 TCACCGAAGCTAATACTCAGTACTATCAGCAAGAAGCCCTCTAAGCTTCGAGGCGAGATTC 355

Db 241 TATCTGAAGCTACACACAGTTTACCAGCAGAGTATCCAAATTTGAGAAGACAAATTC 300

QY 356 GAGATATTCAGAAATTCAAATAGGCATATTTGTTGGGGAATCAGTTGGTTCTTGAACCTTCA 415

Db 301 GAGATATTCAGAAATTCAAACAGGCACATCTTGTGTGAGCACTTGGTTCTCTGAGTCTCA 360

QY 416 AGGAACCTCAAAAACCTAGAGGAGCTTGTGAAAAGGAATCAGCGGTGCCGCTCCAAAA 475

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RESULT 10

BE434089

LOCUS

DEFINITION

EST405167 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA clone cLEGI4H7, mRNA sequence.

ACCESSION

BE434089

VERSION

BE434089.1 GI:9431932

KEYWORDS

EST.

SOURCE

tomato.

ORGANISM

Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;











VERSION BG444639.1 GI:13354291

KEYWORDS

SOURCE EST.

ORGANISM

Gossypium arboreum.  
Gossypium arboreum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.

REFERENCE

AUTHORS 1 (bases 1 to 892)

Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry

,D., Wood,T.C., Leslie,A. and Wilkins,T.A.

TITLE An integrated analysis of the genetics, development, and evolution

JOURNAL of the cotton fiber

COMMENT Unpublished (2000)

Contact: Wing RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Seq primer: TAATAGGACTCACTATAGGG

High quality sequence start: 6

High quality sequence stop: 685.

FEATURES

source

1..892

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/clone="CA\_Ea0025A08f"

/clone\_lib="Gossypium arboreum 7-10 dpa fiber library"

/tissue\_type="Fibers isolated from bolls harvested 7-10

dpa"

/lab\_host="E. coli"

/note="Vector: pBK-CMV; Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT 303 a 161 c 192 g 223 t

ORIGIN

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Matches 384; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

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QY 166 TGTGATCCGGAAGTTCCTCGTCACTCTTCCACTCGTGGCCCTCTCTATGATACGCC 225

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Db 269 AACACAACTAAGATCAACAATACACAGGTACAGAGGCTTGTCTAGATCTCTAAC 328

QY 286 CTTCTTCCGTCACCGAAGCTAATCTACTACTACTATCAGCAAGAGCCCTTAAGCTTCGG 345

Db 329 ACAACACTCTTACTGAAATCAATGCTCTGATTTATCAACAAGAAATCAGCCAGTTGAG 388

QY 346 AGGAGATTCGAGATATTCAGAAATCAATAGGCATATTTTGGGCAATCATTGGTTCC 405

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QY 406 TTGAATTCAGGAACTCAAAAAGTACAGGACCTCTGTAAGAAAGGAATCAGCCGTGTC 465

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Db 629 CAGG 632

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Job time : 1633.91 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 2, 2003, 06:43:28 ; Search time 50.234 Seconds  
(without alignments)  
8013.329 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1          | 896   | 100.0       | 896    | 9 US-09-978-729A-3    | Sequence 3, Appli  |
| 2          | 896   | 100.0       | 896    | 9 US-09-981-087A-3    | Sequence 3, Appli  |
| 3          | 896   | 100.0       | 896    | 9 US-09-978-382A-3    | Sequence 3, Appli  |
| 4          | 896   | 100.0       | 896    | 9 US-09-978-740A-3    | Sequence 3, Appli  |
| 5          | 896   | 100.0       | 896    | 10 US-09-978-730-3    | Sequence 3, Appli  |
| 6          | 536.8 | 59.9        | 959    | 9 US-09-978-729A-5    | Sequence 5, Appli  |
| 7          | 536.8 | 59.9        | 959    | 9 US-09-981-087A-5    | Sequence 5, Appli  |
| 8          | 536.8 | 59.9        | 959    | 9 US-09-978-382A-5    | Sequence 5, Appli  |
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| 12         | 166.6 | 18.6        | 645    | 9 US-09-938-842A-1776 | Sequence 1776, Ap  |
| 13         | 166.6 | 18.6        | 645    | 9 US-09-853-450-33    | Sequence 33, Appli |
| 14         | 149.2 | 16.7        | 1062   | 9 US-09-978-729A-1    | Sequence 1, Appli  |
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| 21 | 131.2 | 14.6 | 747  | 9  | US-09-853-450-27    | Sequence 27, Appli |
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| 23 | 128.6 | 14.4 | 794  | 9  | US-09-853-450-3     | Sequence 3, Appli  |
| 24 | 127.6 | 14.2 | 753  | 9  | US-09-853-450-29    | Sequence 29, Appli |
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| 29 | 122   | 13.6 | 1057 | 9  | US-09-853-450-1     | Sequence 1, Appli  |
| 30 | 120.4 | 13.4 | 777  | 9  | US-09-938-842A-1873 | Sequence 1873, Ap  |
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| 32 | 110.6 | 12.3 | 633  | 9  | US-09-853-450-35    | Sequence 35, Appli |
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ALIGNMENTS

RESULT 1

US-09-978-729A-3  
; Sequence 3, Application US/09978729A  
; Patent No. US20020178465A1  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin F.  
; APPLICANT: Liljegren, Sarah  
; TITLE OF INVENTION: The Regents of the University of California  
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 19452A-000950US  
; CURRENT APPLICATION NUMBER: US/09/978,729A  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: US 60/090,649  
; PRIOR FILING DATE: 1998-06-25  
; PRIOR APPLICATION NUMBER: US 09/339,998  
; PRIOR FILING DATE: 1999-06-25  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 896  
; TYPE: DNA  
; ORGANISM: Arabidopsis sp.  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (7)..(753)  
; OTHER INFORMATION: AGAMOUS-LIKE 1 (AGL1)  
US-09-978-729A-3

Query Match 100.0%; Score 896; DB 9; Length 896;  
Best Local Similarity 100.0%; Pred. No. 3.5e-257;  
Matches 896; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|    |     |                                                              |     |
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RESULT 2  
US-09-981-087A-3  
; Sequence 3, Application US/09981087A  
; Patent No. US20020178466A1  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin F.  
; APPLICANT: Liljegin, Sarah  
; APPLICANT: Farrandiz, Cristina  
; TITLE OF INVENTION: The Regents of the University of California  
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 19452A-000940US  
; CURRENT APPLICATION NUMBER: US/09/981,087A  
; CURRENT FILING DATE: 2002-05-21  
; PRIOR APPLICATION NUMBER: US 60/090,649  
; PRIOR FILING DATE: 1998-06-25  
; PRIOR APPLICATION NUMBER: US 09/339,998  
; PRIOR FILING DATE: 1999-06-25  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3

; LENGTH: 896  
; TYPE: DNA  
; ORGANISM: Arabidopsis sp.  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (7)..(753)  
; OTHER INFORMATION: AGAMOUS-LIKE 1 (AGL1)  
US-09-981-087A-3

Query Match 100.0%; Score 896; DB 9; Length 896;  
Best Local Similarity 100.0%; Pred. No. 3.5e-257;  
Matches 896; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATCAATGGAGGAGGTGGGAGTAGTCAGCACCGCAGAGAGTAGCAAGAACTAGGGAGA 60  
Db 1 GGATCAATGGAGGAGGTGGGAGTAGTCAGCACCGCAGAGAGTAGCAAGAACTAGGGAGA 60  
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QY 841 ATTCATAGTTTAGGTTCTTAATGATAATAACAAAACCTGTTGTTCTTTGCTTCA 896  
Db 841 ATTCATAGTTTAGGTTCTTAATGATAATAACAAAACCTGTTGTTCTTTGCTTCA 896

## RESULT 3

US-09-978-382A-3  
; Sequence 3, Application US/09978382A  
; Publication No. US20020194647A1  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin F.  
; APPLICANT: Liljegren, Sarah  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 19452A-000930US  
; CURRENT APPLICATION NUMBER: US/09/978,382A  
; CURRENT FILING DATE: 2002-06-18  
; PRIOR APPLICATION NUMBER: US 60/090,649  
; PRIOR FILING DATE: 1998-06-25  
; PRIOR APPLICATION NUMBER: US 09/339,998  
; PRIOR FILING DATE: 1999-06-25  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 896  
; TYPE: DNA  
; ORGANISM: Arabidopsis sp.  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (7)..(753)  
; OTHER INFORMATION: AGAMOUS-LIKE 1 (AGL1)  
US-09-978-382A-3

Query Match 100.0%; Score 896; DB 9; Length 896;  
Best Local Similarity 100.0%; Pred. No. 3.5e-257;  
Matches 896; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGATCAATGGAGGAGTGGGAGTAGTCACGAGCAGAGAGTAGCAAGAACTAGGGAGA 60  
Db 1 GGATCAATGGAGGAGTGGGAGTAGTCACGAGCAGAGAGTAGCAAGAACTAGGGAGA 60  
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## RESULT 4

US-09-978-740A-3  
; Sequence 3, Application US/09978740A  
; Publication No. US20030005481A1  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin F.  
; APPLICANT: Liljegren, Sarah  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 19452A-000960US  
; CURRENT APPLICATION NUMBER: US/09/978,740A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: US 60/090,649  
; PRIOR FILING DATE: 1998-06-25  
; PRIOR APPLICATION NUMBER: US 09/339,998  
; PRIOR FILING DATE: 1999-06-25  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 896  
; TYPE: DNA  
; ORGANISM: Arabidopsis sp.  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (7)..(753)  
; OTHER INFORMATION: AGAMOUS-LIKE 1 (AGL1)  
US-09-978-740A-3

Query Match 100.0%; Score 896; DB 9; Length 896;  
Best Local Similarity 100.0%; Pred. No. 3.5e-257;  
Matches 896; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGATCAATGGAGGAGTGGGAGTAGTCACGAGCAGAGAGTAGCAAGAACTAGGGAGA 60  
Db 1 GGATCAATGGAGGAGTGGGAGTAGTCACGAGCAGAGAGTAGCAAGAACTAGGGAGA 60  
QY 61 GGGAAAATAGAGATAAAGAGGATAGAGAACACAAATCGTCAAGTTACTTCTGCAAA 120  
Db 61 GGGAAAATAGAGATAAAGAGGATAGAGAACACAAATCGTCAAGTTACTTCTGCAAA 120  
QY 121 CGACGCAATGGTCTTCTCAAGAAAGCTTATGAATCTCTGTGTGTGATGCCGAAGTT 180  
Db 121 CGACGCAATGGTCTTCTCAAGAAAGCTTATGAATCTCTGTGTGTGATGCCGAAGTT 180  
QY 181 GCCCTCGTCATCTCTCCACTCGTGGCGTCTCTATGAGTACGCCAACACAGTGTGAGG 240  
Db 181 GCCCTCGTCATCTCTCCACTCGTGGCGTCTCTATGAGTACGCCAACACAGTGTGAGG 240  
QY 241 GGTACAATTGAAGGTACAAGAAAGCTTGTTCGGATGCCGTCAACCTCTCTCCGTCAAC 300  
Db 241 GGTACAATTGAAGGTACAAGAAAGCTTGTTCGGATGCCGTCAACCTCTCTCCGTCAAC 300

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Db 241 GGTACAATTGAAAGGTACAAGAAAGCTTGTTCGATGCCGTCAACCCCTCCTCCGTCAAC 300
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Db 301 GAAGCTAATTAAGTACTATACAGCAAGAGCTTCTAGCTTCGGAGGAGAGATTCGAGAT 360
QY 361 ATTCAAGAAATCAATAGGATATGTTGGGGAATCAGTTCCTTGAACCTTCAAGGAA 420
Db 361 ATTCAAGAAATCAATAGGATATGTTGGGGAATCAGTTCCTTGAACCTTCAAGGAA 420
QY 421 CTCAAAAACCTAGAGGAGCTCTTGAAAAAGGAATCAGCCGTCTCCGCTCCAAAAAGAA 480
Db 421 CTCAAAAACCTAGAGGAGCTCTTGAAAAAGGAATCAGCCGTCTCCGCTCCAAAAAGAA 480
QY 481 GAGCTGTTAGTGGCAGAGATAGATATATGCAGAGAGGGAATGGAGTTGCAACACAAT 540
Db 481 GAGCTGTTAGTGGCAGAGATAGATATATGCAGAGAGGGAATGGAGTTGCAACACAAT 540
QY 541 AACATGTACCTGCGAGCAAGATAGCCGAGGCGGAGATTTACGAATCCGGTGTATCTTCTCATGACCCAGTCG 600
Db 541 AACATGTACCTGCGAGCAAGATAGCCGAGGCGGAGATTTACGAATCCGGTGTATCTTCTCATGACCCAGTCG 600
QY 601 TCGAGTGTGATACAGGAGGAGACAGTTCAGCAATCCGGTGTATCTTCTCATGACCCAGTCG 660
Db 601 TCGAGTGTGATACAGGAGGAGACAGTTCAGCAATCCGGTGTATCTTCTCATGACCCAGTCG 660
QY 661 CAGCATTAATCGGAACCTATATTCGGGTGAACCTCTTGAAACCGGAATCAGCAATTCCTCC 720
Db 661 CAGCATTAATCGGAACCTATATTCGGGTGAACCTCTTGAAACCGGAATCAGCAATTCCTCC 720
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Db 721 GGCCAAAGACCAACCTCTCTCAACTTGTGTAACCAACATGATAACTTGTTCCTCC 780
QY 781 CCTCATTAACGATTAAAGAGAGAGAGAGAGTTCATTTTATATTTTATATTAACGCGACTGTGT 840
Db 781 CCTCATTAACGATTAAAGAGAGAGAGAGAGTTCATTTTATATTTTATATTAACGCGACTGTGT 840
QY 841 ATTCATAGTTTAGGTTCTAATAATGATAATAAACAACCTTGTTCCTTCTTCA 896
Db 841 ATTCATAGTTTAGGTTCTAATAATGATAATAAACAACCTTGTTCCTTCTTCA 896

RESULT 5
US-09-978-730-3
; Sequence 3, Application US/09978730
; Patent No. US20020129403A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegen, Sarah
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; FILE OF INVENTION: Plants
; FILE REFERENCE: 19452A-000920US
; CURRENT APPLICATION NUMBER: US/09/978,730
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 896
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(753)
; OTHER INFORMATION: AGAMOUS-LIKE 1 (AGL1)
US-09-978-730-3
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Best Local Similarity 100.0%; Pred. No. 3.5e-257;
Matches 896; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATCAATGGAGAAAGGTGGGAGTAGTCAACGAGCAGAGTAGCAAGAAACTAGGAGA 60
Db 1 GGATCAATGGAGAAAGGTGGGAGTAGTCAACGAGCAGAGTAGCAAGAAACTAGGAGA 60
QY 61 GGGAAAAATAGAGATAAAGAGGATAGAGAAACAACAATACTGTCAGTTACTTCTGAAA 120
Db 61 GGGAAAAATAGAGATAAAGAGGATAGAGAAACAACAATACTGTCAGTTACTTCTGAAA 120
QY 121 CGACGCAATGGTCTCTCAAGAAAGCTTATGAATCTCTGTCTTGTGTGATGCCGAAGTT 180
Db 121 CGACGCAATGGTCTCTCAAGAAAGCTTATGAATCTCTGTCTTGTGTGATGCCGAAGTT 180
QY 181 GCCCTCGTCATCTTCTCCACTCGTGGCGCTCTCTATGATAGCCCAACAACAGTGTGAGG 240
Db 181 GCCCTCGTCATCTTCTCCACTCGTGGCGCTCTCTATGATAGCCCAACAACAGTGTGAGG 240
QY 241 GGTACAATTTGAAGGTACAAGAAAGCTTGTTCGGATGCCGTCAACCCCTCTTCCGTCAAC 300
Db 241 GGTACAATTTGAAGGTACAAGAAAGCTTGTTCGGATGCCGTCAACCCCTCTTCCGTCAAC 300
QY 301 GAAGCTAATTAAGTACTATACAGCAAGAGCTCTTAAAGCTTCGGAGGAGATTCGAGAT 360
Db 301 GAAGCTAATTAAGTACTATACAGCAAGAGCTCTTAAAGCTTCGGAGGAGATTCGAGAT 360
QY 361 ATTCAAGAAATCAATAGGATATGTTGGGGAATCAGTTCGGTTCCTTGAACCTTCAAGGAA 420
Db 361 ATTCAAGAAATCAATAGGATATGTTGGGGAATCAGTTCGGTTCCTTGAACCTTCAAGGAA 420
QY 421 CTCAAAAACCTAGAGGAGCTCTTGAAAAAGGAATCAGCCGTCTCCGCTCCAAAAAGAA 480
Db 421 CTCAAAAACCTAGAGGAGCTCTTGAAAAAGGAATCAGCCGTCTCCGCTCCAAAAAGAA 480
QY 481 GAGCTGTTAGTGGCAGAGATAGATATATGCAGAGAGGGAATGGAGTTGCAACACAAT 540
Db 481 GAGCTGTTAGTGGCAGAGATAGATATATGCAGAGAGGGAATGGAGTTGCAACACAAT 540
QY 541 AACATGTACCTGCGAGCAAGATAGCCGAGGCGGAGATTTACGAATCCGGTGTATCTTCTCATGACCCAGTCG 600
Db 541 AACATGTACCTGCGAGCAAGATAGCCGAGGCGGAGATTTACGAATCCGGTGTATCTTCTCATGACCCAGTCG 600
QY 601 TCGAGTGTGATACAGGAGGAGACAGTTCAGCAATCCGGTGTATCTTCTCATGACCCAGTCG 660
Db 601 TCGAGTGTGATACAGGAGGAGACAGTTCAGCAATCCGGTGTATCTTCTCATGACCCAGTCG 660
QY 661 CAGCATTAATCGGAACCTATATTCGGGTGAACCTCTTGAAACCGGAATCAGCAATTCCTCC 720
Db 661 CAGCATTAATCGGAACCTATATTCGGGTGAACCTCTTGAAACCGGAATCAGCAATTCCTCC 720
QY 721 GGCCAAAGACCAACCTCTCTCAACTTGTGTAACCAACATGATAACTTGTTCCTCC 780
Db 721 GGCCAAAGACCAACCTCTCTCAACTTGTGTAACCAACATGATAACTTGTTCCTCC 780
QY 781 CCTCATTAACGATTAAAGAGAGAGAGAGTTCATTTTATATTTTATATTAACGCGACTGTGT 840
Db 781 CCTCATTAACGATTAAAGAGAGAGAGAGTTCATTTTATATTTTATATTAACGCGACTGTGT 840
QY 841 ATTCATAGTTTAGGTTCTAATAATGATAATAAACAACCTTGTTCCTTCTTCA 896
Db 841 ATTCATAGTTTAGGTTCTAATAATGATAATAAACAACCTTGTTCCTTCTTCA 896

RESULT 6
US-09-978-729A-5
; Sequence 5, Application US/09978729A
; Patent No. US20020178465A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegen, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
```

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; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-0009500S
; CURRENT APPLICATION NUMBER: US/09/978,729A
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 959
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (78)..(818)
; OTHER INFORMATION: AGAMOUS-LIKE 5 (AGL5)
US-09-978-729A-5

Query Match          59.9%; Score 536.8; DB 9; Length 959;
Best Local Similarity 82.1%; Pred. No. 4.2e-150;
Matches 632; Conservative 0; Mismatches 132; Indels 6; Gaps 1;

QY 6 AATGGAGAGGTGGGAGTAGTCACGAGCAGAGAGTAGCAAGAACTAGGGAGAGGGAA 65
Db 77 AATGGAGGGTGGTGGAGTAATGAAGTAGCAGAGCAGCAAGAGATAGGGAGAGGGAA 136

QY 66 AATAGAGATAAGAGGATAGAGAACACAAATCGTCAAGTTACTTTCTGCAACGACG 125
Db 137 GATAGAGATAAGAGGATAGAGAACACTACGAATCGTCAAGTCATTTCTGCAACGACG 196

QY 126 CAATGGTCTTCTCAAGAAAGCTTATGAACCTCTCTGTGTGTGATGCCGAAGTTGCCCT 185
Db 197 CAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGTGTGTGATGCCGTGCTCT 256

QY 186 CGTCATCTTCTCCACTCGTGCGCGTCTCTATGAGTACGCCAACACACAGTGTGAGGGTAC 245
Db 257 TGTCACTCTTCCACTCGAGGCCGCTCTACGAGTACGCCAACACACAGTGTGAGAGAAC 316

QY 306 TAATACTCAGTACTATCAGCAAGAGCCCTTAAGCTTCGAGGAGGATTCGAGATATCA 365
Db 377 TAATACTCAGTACTATCAGCAAGAGCCGCTTAAGCTTCGAGGATTCGAGATATCA 436

QY 366 GAATTCAAATAGGCATATTTGGGGAATCACTTGGTTCCTTGAACCTCAAGGAACCTCAA 425
Db 437 GAATTTGAACAGACACATTTCTTGGTGAATCTCTTGGTTCCTTGAACCTTAAAGGAACCTCAA 496

QY 426 AAACCTAGAGGAGCGTCTTGAAGAAAGGAATCAGCCGTGCTCCGCTCCCAAGAAATGAGCT 485
Db 497 GAACCTTGAAGAGTAGGCTTGAGAAAGGAATCAGTCGTGCTCCGATCCCAAGAACGAGAT 556

QY 486 GTTAGTGCAGAGATAGATATATGCAGAGAGGGAAATGGAGTTGCAACACAATACAT 545
Db 557 GTTAGTGCAGAGATTAATATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 616

QY 546 GTACCTGCGAGCAAGATAGCCGAGGCGCAGATTGAATCCGGACACGAGGAATTCGAG 605
Db 617 GTATCTCCGCTCCCAAGATTACTGAA-----AGAACAGGCTTACAGCAACAGAAATCGAG 670

QY 606 TGTGATACAGGGACACAGTTTACGAATCCGGTGPATCTTCTCATGACCAAGTCGAGCA 665
Db 671 TGTGATACATCAAGGACAGTTTACGAGTCGGGTGTACTTCTTCTCACCAGTCGGGGCA 730

QY 666 TTATAATCGGAACATATATTCGGGTGAACCTTCTTTGAACCGGAATCAGCAATTTCTCCGGCCA 725
Db 731 GTATAACCGGAATTAATATTCGGGTGAACCTTCTTTGAACCGGAATCAGCAATTTCTCCAAACCA 790

QY 726 AGACCAACCTCTCTCAACTTGTGTAACCTCAAAACATGATAACTTGTTT 775
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Db 791 AGACCAACCACTCTGCAACTGTTTTCATTTCAGTCTAACATAAGCTTCTT 840

RESULT 7
US-09-981-087A-5
; Sequence 5, Application US/09981087A
; Patent No. US20020178466A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegren, Sarah
; APPLICANT: Farrandiz, Cristina
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-0009400S
; CURRENT APPLICATION NUMBER: US/09/981,087A
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 959
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (78)..(818)
; OTHER INFORMATION: AGAMOUS-LIKE 5 (AGL5)
US-09-981-087A-5
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Query Match          59.9%; Score 536.8; DB 9; Length 959;
Best Local Similarity 82.1%; Pred. No. 4.2e-150;
Matches 632; Conservative 0; Mismatches 132; Indels 6; Gaps 1;

QY 6 AATGGAGAGGTGGGAGTAGTCACGAGCAGAGAGTAGCAAGAACTAGGGAGAGGGAA 65
Db 77 AATGGAGGGTGGTGGAGTAATGAAGTAGCAGAGCAGCAAGAGATAGGGAGAGGGAA 136

QY 66 AATAGAGATAAGAGGATAGAGAACACAAATCGTCAAGTTACTTTCTGCAACGACG 125
Db 137 GATAGAGATAAGAGGATAGAGAACACTACGAATCGTCAAGTCATTTCTGCAACGACG 196

QY 126 CAATGGTCTTCTCAAGAAAGCTTATGAACCTCTCTGTGTGTGATGCCGAAGTTGCCCT 185
Db 197 CAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGTGTGTGATGCCGTGCTCT 256

QY 186 CGTCATCTTCTCCACTCGTGCGCGTCTCTATGAGTACGCCAACACACAGTGTGAGGGTAC 245
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QY 246 AATGAAAGGTACAGAAAGCTTGTTCGGATGCCGTCAACCCTCCTTCCTCACCAGAGC 305
Db 317 AATAGAAAGGTACAGAAAGCTTGTTCGGATGCCGTCAACCCTCCTTCCTCACCAGAGC 376

QY 306 TAATACTCAGTACTATCAGCAAGAGCCCTTAAGCTTCGAGGAGGATTCGAGATATCA 365
Db 377 TAATACTCAGTACTATCAGCAAGAGCCGCTTAAGCTTCGAGGATTCGAGATATCA 436

QY 366 GAATTCAAATAGGCATATTTGGGGAATCACTTGGTTCCTTGAACCTCAAGGAACCTCAA 425
Db 437 GAATTTGAACAGACACATTTCTTGGTGAATCTCTTGGTTCCTTGAACCTTAAAGGAACCTCAA 496

QY 426 AAACCTAGAGGAGCGTCTTGAAGAAAGGAATCAGCCGTGCTCCGCTCCCAAGAAATGAGCT 485
Db 497 GAACCTTGAAGAGTAGGCTTGAGAAAGGAATCAGTCGTGCTCCGATCCCAAGAACGAGAT 556

QY 486 GTTAGTGCAGAGATAGATATATGCAGAGAGGGAAATGGAGTTGCAACACAATACAT 545
Db 557 GTTAGTGCAGAGATTAATATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 616
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Db 197 CAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGTCTTGTGTGACGCTGAGGTTGCTCT 256  
QY 186 CGTCATCTTCTCCACTCGTGGCCGCTCTATGAGTACGCCAACACACAGTGTGAGGGGTAC 245  
Db 257 TGTCTATCTTCTCCACTCGAGCGGCTCTTACGAGTACGCCAACACACAGTGTGAGAGAAC 316  
QY 246 AATTGAAAGGTACAGAAAGCTTGTTCGGATGCCGTCAACCCCTCTTCCGTACCCGAAGC 305  
Db 317 AATGAAAGGTACAGAAAGCTTGTTCGGATGCCGTCAACCCCTCTTCCGTACCCGAAGC 376  
QY 306 TAATCTACTAGTACTATCAGCAAGAGCCTTAAGCTTCGGAGGACAGATTTCGAGATATTCA 365  
Db 377 TAATCTACTAGTACTATCAGCAAGAGCCTTAAGCTTCGGAGGACAGATTTCGAGATATTCA 436  
QY 366 GAATTCAAATAGGCATATTGTTGGGGAATCACCTTGGTTCCTTGAACCTTCAAGGAACCTCAA 425  
Db 437 GAATTTGAACAGACACATCTTGGTGAATCTCTTGGTTCCTTGAACCTTCAAGGAACCTCAA 496  
QY 426 AAACCTAGAGGACGCTCTTGAAAGAGGAATCAGCGGTGTCCGCTCCCAAAAGAAATGAGCT 485  
Db 497 GAACCTTGAAAGTAGGCTTGAGAAAGGAATCAGTGTGTCCGATCCCAAGAACGACGAGAT 556  
QY 486 GTTAGTGGCAGAGATAGATATATGCAGAGAGGAGGAAATGGAGTTGCAACACAAATAACAT 545  
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QY 606 TGTGATACAGGACGACAGTGTACGAATCCGGTGAACCTTCTTGAACCGAATCAGCAATTCCTCCGGCCA 665  
Db 671 TGTGATACATCAAGGACAGTTTACGAGTGGGTGTTACTTCTTCTACCCAGTCGGGGCA 730  
QY 731 GTATAACCGGAATATATATTCGGGTTAACTTCTTGAACCGAATCAGAAATTCCTCCAACCA 790  
QY 726 AGACCAACCTCCTCTCAACTTGTGTAACCTCAAAACATGATAACTTGT 775  
Db 791 AGACCAACCACTCTGCAACTTGTGTAACCTTGTGTAACCTCAAAACATGATAACTTGT 840

RESULT 10

US-09-978-730-5  
; Sequence 5, Application US/09978730  
; Patent No. US20020129403A1  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin F.  
; APPLICANT: Liljegen, Sarah  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic  
; FILE OF INVENTION: Plants  
; FILE REFERENCE: 19452A-000920US  
; CURRENT APPLICATION NUMBER: US/09/978,730  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: US 60/090,649  
; PRIOR FILING DATE: 1998-06-25  
; PRIOR APPLICATION NUMBER: US 09/339,998  
; PRIOR FILING DATE: 1999-06-25  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 959  
; TYPE: DNA  
; ORGANISM: Arabidopsis sp.  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (78)..(818)  
; OTHER INFORMATION: AGAMOUS-LIKE 5 (AGL5)  
US-09-978-730-5

Query Match 59.9%; Score 536.8; DB 10; Length 959;  
Best Local Similarity 82.1%; Pred. No. 4.2e-150;  
Matches 632; Conservative 0; Mismatches 132; Indels 6; Gaps 1;

QY 6 AATGGAGGAAGTGGGAGTAGTCACGACGACAGAGTAGCAAGAACTAGGGAGAGGGAA 65  
Db 77 AATGGAGGGTGGTGGAGTAATGAAGTAGCAGAGACGCAAGAAGATAGGGAGAGGGAA 136  
QY 66 AATAGAGATAAAGAGGATAGAGAACACAAATCGTCAAGTTACTTTCTGCAACGACG 125  
Db 137 GATAGAGATAAAGAGGATAGAGAACACATACGAATCGTCAAGTCACTTTCTGCAACGACG 196  
QY 126 CAATGGTCTTCTCAAGAAAGCTTATGAACCTCTCTGTCTGTGTGATCGCAAGTTGCCCT 185  
Db 197 CAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGTCTGTGTGACGCTGAGGTTGCTCT 256  
QY 186 CGTCATCTTCTCCACTCGTGGCGTCTCTATGAGTACGCCAACACAGTGTGAGGGGTAC 245  
Db 257 TGTCTATCTTCTCCACTCGAGGCGTCTCTACGAGTACGCCAACACAGTGTGAGAGGAAC 316  
QY 246 AATGAAAGGTACAAAGAAAGCTTGTTCGGATGCCGTCAACCCCTCTTCCGTACCCGAAGC 305  
Db 317 AATGAAAGGTACAAAGAAAGCTTGTTCGGATGCCGTCAACCCCTCTTCCGTACCCGAAGC 376  
QY 306 TAATCTACTAGTACTATCAGCAAGAGCCTCTAAGCTTCGGAGGACAGATTTCGAGATATTCA 365  
Db 377 TAATCTACTAGTACTATCAGCAAGAGGCGTCTAACTCCGGAGACAGATTTCGGACATTCA 436  
QY 366 GAATTCAAATAGGCATATTGTTGGGGAATCACCTTGGTTCCTTGAACCTTCAAGGAACCTCAA 425  
Db 437 GAATTTGAACAGACACATCTTGGTGAATCTCTTGGTTCCTTGAACCTTCAAGGAACCTCAA 496  
QY 426 AAACCTAGAGGACGCTCTTGAAAGAGGAATCAGCGGTGTCCGCTCCCAAAAGAAATGAGCT 485  
Db 497 GAACCTTGAAAGTAGGCTTGAGAAAGGAATCAGTGTGTCCGATCCCAAGAACGACGAGAT 556  
QY 486 GTTAGTGGCAGAGATAGATATATGCAGAGAGGAGGAAATGGAGTTGCAACACACATAACAT 545  
Db 557 GTTAGTTGCAGAGATGAATACATGCAAAAAGGAAATCGAGCTGCAAAACGATAACAT 616  
QY 546 GTACCTGCGAGCAAGATAGCCGAGGCGCCAGATGAATCCGACACGAGGAATCGAG 605  
Db 617 GTATCTCCGCTCCAGATTACTGAA-----AGAACAGGTCTACAGCAACAAGATCGAG 670  
QY 606 TGTGATACAGGACGACAGTGTACGAATCCGGTGTATCTTCTCATGACCACTGCGACGA 665  
Db 671 TGTGATACATCAAGGACAGTTTACGAGTGGGTGTTACTTCTTCTACCCAGTCGGGGCA 730  
QY 666 TTATAATCGGAACACTATATTCGGTGAACCTTCTTGAACCGAATCAGCAATTCCTCCGGCCA 725  
Db 731 GTATAACCGGAATATATTCGGGTTAACTTCTTGAACCGAATCAGAAATTCCTCCAACCA 790  
QY 726 AGACCAACCTCCTCTCAACTTGTGTAACCTCAAAACATGATAACTTGT 775  
Db 791 AGACCAACCACTCTGCAACTTGTGTAACCTTGTGTAACCTCAAAACATGATAACTTGT 840

RESULT 11

US-09-770-445-644/c  
; Sequence 644, Application US/09770445  
; Patent No. US20020023281A1  
; GENERAL INFORMATION:  
; APPLICANT: Goralach, Jörn  
; APPLICANT: An, Yong-Qiang  
; APPLICANT: Hamilton, Carol M.  
; APPLICANT: Price, Jennifer L.  
; APPLICANT: Raines, Tracy M.  
; APPLICANT: Yu, Yang  
; APPLICANT: Rameaka, Joshua G.  
; APPLICANT: Page, Amy  
; APPLICANT: Matthew, Abraham V.  
; APPLICANT: Ledford, Brooke L.  
; APPLICANT: Woessner, Jeffrey P.

```

; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kriker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2023US (PARA-012PRV)
; CURRENT APPLICATION NUMBER: US/09/770,445
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,472
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 644
; LENGTH: 845
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; ORGANISM: Arabidopsis thaliana
US-09-770-445-644

Query Match      21.9%; Score 196.2; DB 10; Length 845;
Best Local Similarity 66.4%; Pred. No. 1.3e-48;
Matches 282; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

QY 176 AAGTTGCCCTCGTCATCTTCCACTCGTGGCGGCTCTATGAGTACGCCCAACACAGTG 235
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Db 845 AAGTTGCCCTCATTTGTTTCCACTCGTGGCGGCTCTATGAATACGCCCAATAACA 786

QY 236 TGAGGGGTACAAATGAAAGGTACAAAGGCTTGTTCCGATGCCGTCAACCCCTCTCCG 295
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 785 TAAGTCAACCATTTGAGAGGTACAAAGGCTTGTTCTGATAGCACCACACTAGCACTG 726

QY 296 TCACCGAAGCTAACTACACTCAGTACTATCAGCAAGAAGCCTCTAAGCTTCGGAGGCAGATTC 355
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 725 TCCAAGAAATCAATGCCGCTACTATCAACAAGAATCTGCTAAGCTGAGACAACAGATCC 666

QY 356 GAGATATTCAGAAATTCAAATAGGCATATTGTTGGGAATCACTTGCTTCCCTGAACTTCA 415
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 665 AAACGATTCAAACTCAACAGGAATCTGATGGGAGACTCTTTGAGTTCCCTTAAGTGCA 606

QY 416 AGGAACTCAAAACCTAGAAGGACGCTTGTAAGAAAGAAATCAGCCGTGTCGCTCCAAA 475
      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 605 AGGAACTAACAAGTTGAGATCGCCTTGAGAAAGCTATCTTAGGATCAGGTCCAAAGA 546

QY 476 AGAATGAGCTGTAGTGGCAGAGATAGATATATGCAAGAGGGGAAATGGAGTTGCAAC 535
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; Sequence 1776, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SAME, AND METHODS OF USE
; CURRENT APPLICATION NUMBER: US/09/938,842A

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; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1776
; LENGTH: 645
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1776

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RESULT 13
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; Sequence 33, Application US/09853450
; Publication No. US20020194645A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Pelaz, Soraya
; APPLICANT: Ditta, Gary
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; FILE REFERENCE: 19452A-002400US
; CURRENT APPLICATION NUMBER: US/09/853,450
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 61
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GenCore version 5.1.3  
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| 4          | 532.4 | 59.4        | 777    | 21 | AAC43464 Arabidopsis thalia |
| 5          | 335.8 | 37.5        | 5622   | 20 | AAV99857 Arabidopsis AGL1 g |
| 6          | 335.8 | 37.5        | 5622   | 24 | AAH77274 Arabidopsis dehisc |
| 7          | 326.6 | 36.5        | 1143   | 17 | AAT34428 Eucalyptus AGE1 cd |
| 8          | 322   | 35.9        | 511    | 21 | AAC33755 Arabidopsis thalia |
| 9          | 312.6 | 34.9        | 714    | 22 | AAF85402 Nucleotide sequenc |

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| 10 | 312.6 | 34.9 | 1115 | 21 | AAZ57949 Poplar floral home  |
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| 13 | 311.6 | 34.8 | 511  | 21 | AAC45357 Arabidopsis thalia  |
| 14 | 305.2 | 34.1 | 723  | 22 | AAF85399 Nucleotide sequenc  |
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| 29 | 231.8 | 25.9 | 581  | 21 | AAC57270 Eucalyptus grandis  |
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| 36 | 159   | 17.7 | 498  | 20 | AAV69758 Tobacco ovary-spec  |
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| 38 | 157.6 | 17.6 | 352  | 21 | AAC55878 Eucalyptus grandis  |
| 39 | 155   | 17.3 | 423  | 21 | AAC56741 Eucalyptus grandis  |
| 40 | 154.2 | 17.2 | 457  | 21 | AAC41474 Zea mays DNA fragm  |
| 41 | 153   | 17.1 | 1075 | 21 | AAC37803 Arabidopsis thalia  |
| 42 | 149.2 | 16.7 | 1062 | 20 | AAH18594 Arabidopsis AGL8 n  |
| 43 | 149.2 | 16.7 | 1062 | 20 | AAV99856 Arabidopsis AGL8-1  |
| 44 | 147.6 | 16.5 | 1123 | 21 | AAC41877 Arabidopsis thalia  |
| 45 | 143.2 | 16.0 | 1342 | 18 | AAAT99437 Maize floral meris |

ALIGNMENTS

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AC AAV99859;

XX 10-MAY-1999 (first entry)

DT 10-MAY-1999 (first entry)

DE Arabidopsis AGL1 cDNA.

XX Arabidopsis thaliana.

FW Key Location/Qualifiers

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FT /\*tag= b

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PD 07-JAN-1999.

XX 25-JUN-1998; 98WO-US13208.

PR 28-APR-1998; 98US-0067800.

XX 27-JUN-1997; 97US-0051030.

XX (REGC ) UNIV CALIFORNIA.





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| PR                                                             | 28-JUL-1999; | 99US-0145951.                                                       |
| PR                                                             | 02-AUG-1999; | 99US-0146386.                                                       |
| PR                                                             | 02-AUG-1999; | 99US-0146388.                                                       |
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| PR                                                             | 03-AUG-1999; | 99US-0147038.                                                       |
| PR                                                             | 04-AUG-1999; | 99US-0147204.                                                       |
| PR                                                             | 04-AUG-1999; | 99US-0147302.                                                       |
| PR                                                             | 05-AUG-1999; | 99US-0147192.                                                       |
| PR                                                             | 05-AUG-1999; | 99US-0147260.                                                       |
| PR                                                             | 06-AUG-1999; | 99US-0147303.                                                       |
| PR                                                             | 06-AUG-1999; | 99US-0147416.                                                       |
| PR                                                             | 09-AUG-1999; | 99US-0147493.                                                       |
| PR                                                             | 09-AUG-1999; | 99US-0147935.                                                       |
| PR                                                             | 10-AUG-1999; | 99US-0148171.                                                       |
| PR                                                             | 11-AUG-1999; | 99US-0148319.                                                       |
| PR                                                             | 12-AUG-1999; | 99US-0148341.                                                       |
| PR                                                             | 13-AUG-1999; | 99US-0148565.                                                       |
| PR                                                             | 13-AUG-1999; | 99US-0148684.                                                       |
| PR                                                             | 16-AUG-1999; | 99US-0149368.                                                       |
| PR                                                             | 17-AUG-1999; | 99US-0149175.                                                       |
| PR                                                             | 18-AUG-1999; | 99US-0149426.                                                       |
| PR                                                             | 20-AUG-1999; | 99US-0149722.                                                       |
| PR                                                             | 20-AUG-1999; | 99US-0149723.                                                       |
| PR                                                             | 20-AUG-1999; | 99US-0149929.                                                       |
| PR                                                             | 23-AUG-1999; | 99US-0149902.                                                       |
| PR                                                             | 23-AUG-1999; | 99US-0149930.                                                       |
| PR                                                             | 25-AUG-1999; | 99US-0150366.                                                       |
| PR                                                             | 26-AUG-1999; | 99US-0150884.                                                       |
| PR                                                             | 27-AUG-1999; | 99US-0151065.                                                       |
| PR                                                             | 27-AUG-1999; | 99US-0151066.                                                       |
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| PR                                                             | 30-AUG-1999; | 99US-0151303.                                                       |
| PR                                                             | 31-AUG-1999; | 99US-0151438.                                                       |
| PR                                                             | 01-SEP-1999; | 99US-0151930.                                                       |
| PR                                                             | 07-SEP-1999; | 99US-0152363.                                                       |
| PR                                                             | 10-SEP-1999; | 99US-0153070.                                                       |
| PR                                                             | 13-SEP-1999; | 99US-0153758.                                                       |
| PR                                                             | 15-SEP-1999; | 99US-0154018.                                                       |
| PR                                                             | 16-SEP-1999; | 99US-0154039.                                                       |
| PR                                                             | 22-SEP-1999; | 99US-0154779.                                                       |
| PR                                                             | 22-SEP-1999; | 99US-0155139.                                                       |
| PR                                                             | 23-SEP-1999; | 99US-0155486.                                                       |
| PR                                                             | 24-SEP-1999; | 99US-0155659.                                                       |
| PR                                                             | 28-SEP-1999; | 99US-0156458.                                                       |
| PR                                                             | 29-SEP-1999; | 99US-0156596.                                                       |
| PR                                                             | 04-OCT-1999; | 99US-0157117.                                                       |
| PR                                                             | 05-OCT-1999; | 99US-0157753.                                                       |
| PR                                                             | 08-OCT-1999; | 99US-0157865.                                                       |
| PR                                                             | 07-OCT-1999; | 99US-0158029.                                                       |
| PR                                                             | 08-OCT-1999; | 99US-0158232.                                                       |
| PR                                                             | 12-OCT-1999; | 99US-0158369.                                                       |
| PR                                                             | 13-OCT-1999; | 99US-0159293.                                                       |
| PR                                                             | 13-OCT-1999; | 99US-0159294.                                                       |
| PR                                                             | 13-OCT-1999; | 99US-0159295.                                                       |
| PR                                                             | 14-OCT-1999; | 99US-0159329.                                                       |
| PR                                                             | 14-OCT-1999; | 99US-0159330.                                                       |
| PR                                                             | 14-OCT-1999; | 99US-0144352.                                                       |
| PR                                                             | 14-OCT-1999; | 99US-0144632.                                                       |
| PR                                                             | 14-OCT-1999; | 99US-0144884.                                                       |
| PR                                                             | 18-OCT-1999; | 99US-0159584.                                                       |
| PR                                                             | 21-OCT-1999; | 99US-0160741.                                                       |
| PR                                                             | 21-OCT-1999; | 99US-0160767.                                                       |
| PR                                                             | 21-OCT-1999; | 99US-0160768.                                                       |
| PR                                                             | 21-OCT-1999; | 99US-0160770.                                                       |
| PR                                                             | 21-OCT-1999; | 99US-0160814.                                                       |
| PR                                                             | 21-OCT-1999; | 99US-0160815.                                                       |
| PR                                                             | 22-OCT-1999; | 99US-0160980.                                                       |
| PR                                                             | 22-OCT-1999; | 99US-0160981.                                                       |
| PR                                                             | 22-OCT-1999; | 99US-0160989.                                                       |
| PR                                                             | 25-OCT-1999; | 99US-0161404.                                                       |
| PR                                                             | 25-OCT-1999; | 99US-0161405.                                                       |
| PR                                                             | 25-OCT-1999; | 99US-0161406.                                                       |
| PR                                                             | 26-OCT-1999; | 99US-0161359.                                                       |
| PR                                                             | 26-OCT-1999; | 99US-0161360.                                                       |
| PR                                                             | 26-OCT-1999; | 99US-0161361.                                                       |
| PR                                                             | 28-OCT-1999; | 99US-0161920.                                                       |
| PR                                                             | 28-OCT-1999; | 99US-0161992.                                                       |
| PR                                                             | 28-OCT-1999; | 99US-0161993.                                                       |
| PR                                                             | 29-OCT-1999; | 99US-0162142.                                                       |
| Query Match 59.4%; Score 532.4; DB 21; Length 777;             |              |                                                                     |
| Best Local Similarity 81.6%; Pred. No. 3.6e-153;               |              |                                                                     |
| Matches 630; Conservative 0; Mismatches 136; Indels 6; Gaps 1; |              |                                                                     |
| QY                                                             | 7            | ATGGAGGAAGTGGGAGTAGTCACGACCAGAGAGTAGCAAGAAATAGGGAGAGGGA 66          |
| Db                                                             | 1            | ATGGAGGTTGGTGGGAGTAATGAAGTAGCAGAGAGCAGCAAGAAATAGGGAGAGGGA 60        |
| QY                                                             | 67           | ATAGAGATAAAGAGATAGAGAACACACAAATCGTCAAGTACTTTCTGCAACAGCGC 126        |
| Db                                                             | 61           | ATAGAGATAAAGAGATAGAGAACACTACGAATCGTCAAGTCACTTTCTGCAACAGCGC 120      |
| QY                                                             | 127          | AATGGTCTTCTCAAGAAAGCTTATGAACCTCTGTCTGTGTGTGATGCCGAAGTTGCCCTC 186    |
| Db                                                             | 121          | AATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGTCTGTGTGTGATGCCGAAGTTGCCCTT 180   |
| QY                                                             | 187          | GTCATCTTCTCCACTCGTGGCCGCTCTATGATGACGCAACAAACAGTGTAGGGGTACA 246      |
| Db                                                             | 181          | GTCATCTTCTCCACTCGGCGCGTCTCTACGAGTACGCGCAACAAACAGTGTAGAGGACACA 240   |
| QY                                                             | 247          | ATTGAAGGTACAGAAAGCTTGTTCGGATGCCGTCAACCCCTCCTTCGTCACCGAAGCT 306      |
| Db                                                             | 241          | ATAGAAAGGTACAGAAAGCTTGTTCGGACGCGTTAAACCCCTCCGACCATCACCGAAGCT 300    |
| QY                                                             | 307          | AATACTCAGTACTATCAGCAAGAGCCCTTAAGCTTCGAGGCGAGATTCGAGATATTCCAG 366    |
| Db                                                             | 301          | AATACTCAGTACTATCAGCAAGAGCGCTTAACTCCGAGACAGATTCGGGACATTCCAG 360      |
| QY                                                             | 367          | AATCAAAATAGGCATATTGTTGGGAAATCACTTGGTTCCTTGAACCTCAAGGAACACTCAA 426   |
| Db                                                             | 361          | AATTGAACAGACACATCTTGGTGAATCTCTTGGTTCCTTGAACCTTAAAGGAACACTCAAG 420   |
| QY                                                             | 427          | AACCTAGAAGCAGCGTCTTGAAAAAGGAATCAGCGTGTCCGCTCCAAAAAGAAATGAGCTG 486   |
| Db                                                             | 421          | AACCTTGAAGTAGGCTTGAGAAAGGAATCAGCTGTCCGATCCAAAGAGCAGCAGATG 480       |
| QY                                                             | 487          | TTAGTGGCAGATAGATATATGCAGAGAGGGAATAGGAGTTGCAACACAATAAACATG 546       |
| Db                                                             | 481          | TTAGTTCAGAGATTGAATACATGCAAAAAAGGGAATCGAGCTGCAAAACGATAACATG 540      |
| QY                                                             | 547          | TACCTCGCAGAAAGATAGCGGAAGCGCCAGATTGAATCCGACCAGCAGGAATCCGAGT 606      |
| Db                                                             | 541          | TATCTCCGCTCCAAGATTACTGAA-----AGAACAGGTCTACAGCAACAAGAAATCCGAGT 594   |
| QY                                                             | 607          | GTGATACAAAGGACAGATTTACGAATCCGGTGTATCTTCTCATGACCAGTCGCGAGCAT 666     |
| Db                                                             | 595          | GTGATACATCAAGGGACAGTTACGAGTCGGGTGTACTTCTTCTCACCAGTCGGGGCAG 654      |
| QY                                                             | 667          | TATAATCGGAACATATATTCCGGTGAACCTTCTTGAACCGGAATCAGCAATTTCTCCGCCCAA 726 |

|              |                                                                  |                                                                                                            |     |
|--------------|------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------|-----|
| Db           | 655                                                              | TATAACGGGAATTATATTGCGGTAACTTCTTGAACCGAATCAGAATTCCTCCAACCA                                                  | 711 |
| QY           | 727                                                              | GACCAACCTCCTCTTCAACTTGTTGTAACCAAACAATGATAACTGTTTCTT                                                        | 778 |
| Db           | 715                                                              | GACCAACCACCTCTGCAACTTAGGGACCTAATAATTACATATATCTTGATT                                                        | 766 |
| <br>RESULT 5 |                                                                  |                                                                                                            |     |
| ID           | AAV99857 standard; cDNA; 5622 BP.                                |                                                                                                            |     |
| XX           | AAV99857;                                                        |                                                                                                            |     |
| AC           |                                                                  |                                                                                                            |     |
| DT           | 10-MAY-1999 (first entry)                                        |                                                                                                            |     |
| XX           |                                                                  |                                                                                                            |     |
| DE           | Arabidopsis AGLI gene.                                           |                                                                                                            |     |
| XX           |                                                                  |                                                                                                            |     |
| KW           | AGLI-like gene; agamous-like 1 gene; seed dispersal; dehiscence; |                                                                                                            |     |
| KW           | transgenic plant; promoter; ss.                                  |                                                                                                            |     |
| XX           |                                                                  |                                                                                                            |     |
| OS           | Arabidopsis thaliana.                                            |                                                                                                            |     |
| OS           |                                                                  |                                                                                                            |     |
| FH           | Key                                                              | Location/Qualifiers                                                                                        |     |
| FT           | CDS                                                              | 2606..5220                                                                                                 |     |
| FT           |                                                                  | /tag= a                                                                                                    |     |
| FT           |                                                                  | /note= "contains introns"                                                                                  |     |
| FT           | exon                                                             | 1606..2832                                                                                                 |     |
| FT           |                                                                  | /tag= b                                                                                                    |     |
| FT           |                                                                  | /number= 1                                                                                                 |     |
| FT           | intron                                                           | 2833..4128                                                                                                 |     |
| FT           |                                                                  | /tag= c                                                                                                    |     |
| FT           |                                                                  | /number= 1                                                                                                 |     |
| FT           |                                                                  | /note= "this region is specifically claimed in Claim 26 as a dehiscence zone-selective regulatory element" |     |
| FT           | exon                                                             | 4129..4210                                                                                                 |     |
| FT           |                                                                  | /tag= d                                                                                                    |     |
| FT           |                                                                  | /number= 2                                                                                                 |     |
| FT           | intron                                                           | 4211..4363                                                                                                 |     |
| FT           |                                                                  | /tag= e                                                                                                    |     |
| FT           |                                                                  | /number= 2                                                                                                 |     |
| FT           |                                                                  | /note= "this region is specifically claimed in Claim 26 as a dehiscence zone-selective regulatory element" |     |
| FT           | exon                                                             | 4364..4425                                                                                                 |     |
| FT           |                                                                  | /tag= f                                                                                                    |     |
| FT           |                                                                  | /number= 3                                                                                                 |     |
| FT           | intron                                                           | 4426..4554                                                                                                 |     |
| FT           |                                                                  | /tag= g                                                                                                    |     |
| FT           |                                                                  | /number= 3                                                                                                 |     |
| FT           |                                                                  | /note= "this region is specifically claimed in Claim 26 as a dehiscence zone-selective regulatory element" |     |
| FT           | exon                                                             | 4545..4654                                                                                                 |     |
| FT           |                                                                  | /tag= h                                                                                                    |     |
| FT           |                                                                  | /number= 4                                                                                                 |     |
| FT           | intron                                                           | 4655..4753                                                                                                 |     |
| FT           |                                                                  | /tag= i                                                                                                    |     |
| FT           |                                                                  | /number= 4                                                                                                 |     |
| FT           |                                                                  | /note= "this region is specifically claimed in Claim 26 as a dehiscence zone-selective regulatory element" |     |
| FT           | exon                                                             | 4754..4795                                                                                                 |     |
| FT           |                                                                  | /tag= j                                                                                                    |     |
| FT           |                                                                  | /number= 5                                                                                                 |     |
| FT           | intron                                                           | 4796..4878                                                                                                 |     |
| FT           |                                                                  | /tag= k                                                                                                    |     |
| FT           |                                                                  | /number= 5                                                                                                 |     |
| FT           |                                                                  | /note= "this region is specifically claimed in Claim 26 as a dehiscence zone-selective regulatory element" |     |
| FT           | exon                                                             | 4879..4920                                                                                                 |     |

QY 678 CTATATTCGGGTGAACCTTCTTGAACCGAATCAGCAATTCTCGGCCAAGACCAACCTCC 737  
|||||  
Db 5145 CTATATTCGGGTGAACCTTCTTGAACCGAATCAGCAATTCTCGGCCAAGACCAACCTCC 5204  
|||||  
QY 738 TCTTCAACTGTGTAACTCAAAACATGATAACTGTTCTTCCCCTCATAACGATTAA 797  
|||||  
Db 5205 TCTTCAACTGTGTAACTCAAAACATGATAACTGTTCTTCCCCTCATAACGATTAA 5264  
|||||  
QY 798 GAGAGACGAGAGAGTTCATTTTATATTATAACCGGACTGTGTTATTCATAGTTAGGTT 857  
|||||  
Db 5265 GAGAGACGAGAGAGTTCATTTTATATTATAACCGGACTGTGTTATTCATAGTTAGGTT 5324  
|||||  
QY 858 TAATAATGATAATAACAAACTGTTCTTTGCTTCA 896  
|||||  
Db 5325 TAATAATGATAATAACAAACTGTTCTTTGCTTAA 5363  
|||||  
RESULT 6  
AAH77274  
ID AAH77274 standard; DNA; 5622 BP.  
XX  
AC AAH77274;  
XX  
DT 06-FEB-2002 (first entry)  
XX  
DE Arabidopsis dehiscence zone-selective SHP1 regulatory element.  
XX  
KW IND1; indehiscent 1; fruit dehiscence; oil seed rape; SHP1;  
KW ds.  
XX Arabidopsis sp.  
XX OS  
XX PN W0200179517-A2.  
XX PD 25-OCT-2001.  
XX PF 13-APR-2001; 2001WO-US11967.  
XX PR 13-APR-2000; 2000US-0548971.  
XX (REGC ) UNIV CALIFORNIA.  
XX PA Liljegren S, Yanofsky ME;  
XX PI WPI; 2002-034365/04.  
XX DR Isolated nucleic acids for modulating fruit dehiscence in plants,  
XX PT comprises an indehiscent 1 (IND1) polynucleotide sequence -  
XX PS Disclosure; Page 50-54; 58pp; English.  
XX  
XX The sequence represents the Arabidopsis dehiscence zone-selective SHP1  
XX regulatory element. The invention relates to a novel isolated nucleic  
XX acid encoding an IND1 polypeptide. The polynucleotides of the invention  
XX provide a means of modulating fruit dehiscence which is useful for  
XX increased production of crops such as oil seed rape. The IND1 sequences  
XX can be used to prepare expression cassettes useful in a number of  
XX techniques, including inhibiting or suppressing expression.  
XX  
SQ Sequence 5622 BP; 1853 A; 928 C; 907 G; 1927 T; 7 other;  
Query Match 37.5%; Score 335.8; DB 24; Length 5622;  
Best Local Similarity 99.4%; Pred. No. 2.8e-92;  
Matches 337; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 558 AAGATAGCCGAGGCCAGATTGAATCCGGACCAGCAGGAATCGAGTGTGATACAAGG 617  
|||||  
Db 5025 ATAGATAGCCGAGGCCAGATTGAATCCGGACCAGCAGGAATCGAGTGTGATACAAGG 5084  
|||||  
QY 618 GAGCACAGTTTACGAATCCGGTGTATCTTCATGACCGAGTCGCGACATTATATCGGAA 677  
|||||  
Db 5085 GAGCACAGTTTACGAATCCGGTGTATCTTCATGACCGAGTCGCGACATTATATCGGAA 5144  
|||||

QY 678 CTATATTCGGGTGAACCTTCTTGAACCGAATCAGCAATTCTCGGCCAAGACCAACCTCC 737  
|||||  
Db 5145 CTATATTCGGGTGAACCTTCTTGAACCGAATCAGCAATTCTCGGCCAAGACCAACCTCC 5204  
|||||  
QY 738 TCTTCAACTGTGTAACTCAAAACATGATAACTGTTCTTCCCCTCATAACGATTAA 797  
|||||  
Db 5205 TCTTCAACTGTGTAACTCAAAACATGATAACTGTTCTTCCCCTCATAACGATTAA 5264  
|||||  
QY 798 GAGAGACGAGAGAGTTCATTTTATATTATAACCGGACTGTGTTATTCATAGTTAGGTT 857  
|||||  
Db 5265 GAGAGACGAGAGAGTTCATTTTATATTATAACCGGACTGTGTTATTCATAGTTAGGTT 5324  
|||||  
QY 858 TAATAATGATAATAACAAACTGTTCTTTGCTTCA 896  
|||||  
Db 5325 TAATAATGATAATAACAAACTGTTCTTTGCTTAA 5363  
|||||  
RESULT 7  
AAT34428  
ID AAT34428 standard; cDNA; 1143 BP.  
XX  
AC AAT34428;  
XX  
DT 01-OCT-1996 (first entry)  
XX  
DE Eucalyptus AGE1 cDNA.  
XX  
KW Eucalyptus; reproductive gene; AGE1; Arabidopsis; agamous gene;  
KW Antirrhinum; plena gene; sterility; fertility; forest tree;  
KW transgenic plant; flower development; antisense; ribozyme; ss.  
XX  
OS Eucalyptus globulus.  
XX  
FH Key Location/Qualifiers  
FT CDS 154..909  
FT /\*tag= a  
FT /product= AGE-1  
XX  
PN AU9539013-A.  
XX 30-MAY-1996.  
XX 22-NOV-1995; 95AU-0039013.  
XX 22-NOV-1994; 94AU-0009589.  
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
XX Dennis ES, Harcourt RL, Kyozyuka J, Llewellyn D;  
XX Peacock WJ, Southerton S;  
XX  
XX WPI; 1996-278411/29.  
XX P-PSDB; AAR99633.  
XX  
XX Eucalyptus reproductive genes - useful for prodn. of sterile  
XX Eucalyptus trees useful for establishing wood lot plantations or in  
XX re-forestation projects  
XX  
XX Claim 8; Page 29-30; 60pp; English.  
XX  
XX A cDNA clone (AAT34428), designated AGE1, is analogous to the  
XX Arabidopsis agamous (AG) and Antirrhinum plena (PLE) flower  
XX development genes. It was obtd. by PCR amplification of E.  
XX globulus cDNA using primers based on homologous regions of the  
XX Arabidopsis and Antirrhinum genes, followed by a screening of a E.  
XX globulus library. It codes for a protein, AGE-1 (AAR99633), that  
XX shows homology to the AG and PLE proteins. AGE1 is very  
XX highly expressed in mature flower buds. Another cDNA clone,  
XX AGE2 (AAT34432), was also identified. Antisense or ribozyme  
XX constructs of AGE, or of PLE2 and SQE genes (see also AAT34426 and  
XX AAT34429-31), can be used to produce sterile transgenic Eucalyptus  
XX trees by minimising inflorescence.

|    |                                                                         |                                 |
|----|-------------------------------------------------------------------------|---------------------------------|
| SQ | Sequence 1143 BP; 336 A; 244 C; 267 G; 296 T; 0 other;                  |                                 |
|    | Query Match 36.5%; Score 326.6; DB 17; Length 1143;                     |                                 |
|    | Best local Similarity 67.6%; Pred. No. 8.5e-90;                         |                                 |
|    | Matches 490; Conservative 0; Mismatches 229; Indels 6; Gaps 2;          |                                 |
| QY | 55 GGGAGAGGGAATATAGAGATAAGAGGATAGAGACACAAACAATCTCAAGTTACTTTC 114        | OS                              |
|    |                                                                         | XX Arabidopsis thaliana.        |
| Db | 205 GGGAGAGGGAATATAGAGATAAGAGGATCGAGACACAGCAGCGCAGGTCACCTTT 264         | PN EP1033405-A2.                |
| QY | 115 TGAACAACGACGCAATGGCTTCTCAAGAAAGCTTATGAACCTCTCTGTCTTGTGTATGCC 174    | XX 06-SEP-2000.                 |
| Db | 265 TGTAAACGCGGACGCGTGTGTAAGAGGCTTATGAGCTATCGGTGTGTCGATGCT 324          | PF 25-FEB-2000; 2000EP-0301439. |
| QY | 175 GAAGTTGCCCTCGTCATCTTCTCCACTCGTGGCGCTCTCTATGAGTAGCCCAACAACAGT 234    | XX 25-FEB-1999; 99US-0121825.   |
|    |                                                                         | PR 05-MAR-1999; 99US-0123180.   |
| Db | 325 GAAGTGGCCCTTATGTCTCTCGAGCGTGGCAGGCTCTATGAATATGCTTAACAACAGT 384      | PR 09-MAR-1999; 99US-0123548.   |
| QY | 235 GTGAGGGGTACAATTGAAAGGTACAAGAAAGCTTGTCCGATGCCGTCAACCCCTCCTTCC 294    | PR 23-MAR-1999; 99US-0125788.   |
| Db | 385 GTCAGAGGGAACAATTGAGAGGTACAAGAAAGCAAGCAGTGATCTCATCCACAGTCC 444       | PR 25-MAR-1999; 99US-0126264.   |
| QY | 295 GTCACCGAAGCTAATACCTCAGTACTATCAGCAAGAAGCCTCTAAGCTTCGGAGGCAGATT 354   | PR 29-MAR-1999; 99US-0126785.   |
| Db | 445 GTTCTCTGAAGTGAACACTCAGTCTTATCAGCAAGAAGATCCAAAGCTTCGGAGACAGATA 504   | PR 01-APR-1999; 99US-0127462.   |
| QY | 355 CGAGATATTCAGAAATTCAAATAGGCATATTGTTGGGGGAATCATCTGGTTCCTTGAACATTC 414 | PR 06-APR-1999; 99US-0128234.   |
| Db | 505 AGAGAAATCCAGGCTCAAAATAGGCATATTCTAGGTAGGGTATAAGTGATTTGAGCTTC 564     | PR 08-APR-1999; 99US-0128714.   |
| QY | 415 AAGAACTCAAAACCTAGAAGGACGCTCTTGAAAAGGAATCAGCCGTGTCCGCTCCAAA 474      | PR 16-APR-1999; 99US-0129845.   |
| Db | 565 AAGATCTCAAGATCTCGAGAGCAAAATTAGAGAAATCGATCAGCCGAGTTAGATCAAG 624      | PR 19-APR-1999; 99US-0130077.   |
| QY | 475 AAGATGAGCTGTAGTGGCAGAGATAGATATATCAGAAGAGGGAATGGAGTTGCAA 534         | PR 21-APR-1999; 99US-0130449.   |
| Db | 625 AAGATGAGATGCTTTTCCGAGATTGAGTACATCGAAGAGGGAATTTGAGCTGCAA 684         | PR 23-APR-1999; 99US-0130891.   |
| QY | 535 CACAATAACATGTACCTGGCAGCAAAAGATAGCGAAGCGCCAGATTGAATCCGGACCCAG 594    | PR 28-APR-1999; 99US-0131449.   |
| Db | 685 AATGATAACATGTATCTGAGAGCAAAAGATAGTGAGAACGAGAGAGCAACAACAGCAGCAG 744   | PR 30-APR-1999; 99US-0132048.   |
| QY | 595 CAGGAATCGAGTGTATACAAGGACGACAGTTTACGAATCCGCTGTATCTTCTCATGAC 654      | PR 04-MAY-1999; 99US-0132484.   |
| Db | 745 CAGCAAGGAGTGATCATCACTTCAACATGCCGGGATCGTCGCTGTACGAGGCGCTG 804        | PR 05-MAY-1999; 99US-0132485.   |
| QY | 655 CAGTCGCAGCAT---TATATCGGAACATATATCCGGTGAACCTTCTTGAACCGAATCAG 711     | PR 06-MAY-1999; 99US-0132486.   |
| Db | 805 CCGTCTCAGCTGCATACGATCGCAACTTCCTGCAAGTCAATGTCTTGAACCAAAATCAC 864     | PR 06-MAY-1999; 99US-0132487.   |
| QY | 712 CAA---TTCCTCGGCGCAAGACCAACCTCTCTTCAACTTGTGTAACTCAAAACATGATAA 768    | PR 07-MAY-1999; 99US-0132863.   |
| Db | 865 CAATCTTATTCGATCCGACCACACTGCCCTCCAACTCGTCTAATTAAAGCTCAGTTAA 924      | PR 11-MAY-1999; 99US-0134256.   |
| QY | 769 CTTGT 773                                                           | PR 14-MAY-1999; 99US-0134219.   |
| Db | 925 TATGT 929                                                           | PR 14-MAY-1999; 99US-0134221.   |
|    |                                                                         | PR 14-MAY-1999; 99US-0134370.   |
|    |                                                                         | PR 18-MAY-1999; 99US-0134768.   |
|    |                                                                         | PR 19-MAY-1999; 99US-0134941.   |
|    |                                                                         | PR 20-MAY-1999; 99US-0135124.   |
|    |                                                                         | PR 21-MAY-1999; 99US-0135353.   |
|    |                                                                         | PR 24-MAY-1999; 99US-0135629.   |
|    |                                                                         | PR 25-MAY-1999; 99US-0136021.   |
|    |                                                                         | PR 27-MAY-1999; 99US-0136392.   |
|    |                                                                         | PR 28-MAY-1999; 99US-0136782.   |
|    |                                                                         | PR 01-JUN-1999; 99US-0137222.   |
|    |                                                                         | PR 03-JUN-1999; 99US-0137528.   |
|    |                                                                         | PR 04-JUN-1999; 99US-0137502.   |
|    |                                                                         | PR 07-JUN-1999; 99US-0137724.   |
|    |                                                                         | PR 08-JUN-1999; 99US-0138094.   |
|    |                                                                         | PR 10-JUN-1999; 99US-0138540.   |
|    |                                                                         | PR 10-JUN-1999; 99US-0138847.   |
|    |                                                                         | PR 14-JUN-1999; 99US-0139119.   |
|    |                                                                         | PR 16-JUN-1999; 99US-0139452.   |
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|    |                                                                         | PR 17-JUN-1999; 99US-0139492.   |
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|    |                                                                         | PR 18-JUN-1999; 99US-0139459.   |
|    |                                                                         | PR 18-JUN-1999; 99US-0139460.   |
|    |                                                                         | PR 18-JUN-1999; 99US-0139461.   |
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|    |                                                                         | PR 18-JUN-1999; 99US-0139463.   |
|    |                                                                         | PR 18-JUN-1999; 99US-0139750.   |
|    |                                                                         | PR 18-JUN-1999; 99US-0139763.   |
|    |                                                                         | PR 21-JUN-1999; 99US-0139817.   |
|    |                                                                         | PR 22-JUN-1999; 99US-0139899.   |
|    |                                                                         | PR 23-JUN-1999; 99US-0140353.   |
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|    |                                                                         | PR 24-JUN-1999; 99US-0140695.   |
|    |                                                                         | PR 28-JUN-1999; 99US-0140823.   |
|    |                                                                         | PR 29-JUN-1999; 99US-0140991.   |

RESULT 8  
AAC33755  
ID AAC33755 standard; DNA; 511 BP.  
XX  
AC AAC33755;  
XX  
DT 17-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 4200.  
XX  
KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
XX





[illegible]





us-09-978-382a-3.rng

Mon Feb 3 09:46:03 2003

|    |                              |    |              |               |
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| XX | 06-SEP-2000.                 | PR | 02-JUL-1999; | 99US-0142055. |
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| XX |                              | PR | 08-JUL-1999; | 99US-0142803. |
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| XX | 25-FEB-2000; 2000EP-0301439. | PR | 12-JUL-1999; | 99US-0142977. |
|    |                              | PR | 13-JUL-1999; | 99US-0143542. |
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PR 22-SEP-1999; 99US-0155139.
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PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
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PR 14-OCT-1999; 99US-0159637.
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PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 26-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.
PR 29-OCT-1999; 99US-0162142.

Query Match 34.8%; Score 311.6; DB 21; Length 511;
Best Local Similarity 87.4%; Pred. No. 2.3e-85;
Matches 353; Conservative 0; Mismatches 49; Indels 2; Gaps 1;

QY 6 AATGGAGGAGGTGGGAGTAGTCACGACGAGAGAGTAGCAGAACTAGGGAGAGGAA 65
Db 108 AATGGAGGTGGTCCGAGTAAATGAAGTAGCAGAGAGCAGCAAGAAAGATAGGGAGGGAA 167

QY 66 AATGAGATAAAGAGGATAGAGACACAAATCGTCAAGTTACTTCTGCAAAACGACG 125
Db 168 GATGAGATAAAGAGGATAGAGACACTACGAATCGTCAAGTCACTTCTGCAAAACGACG 227

QY 126 CAATGGTCTTCTCAAGAAAGCTTATGAACTCTCTGTCTGTGTGATGCCGAAGTTGCCCT 185
Db 228 CAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGTCTGTGTGACGCTGAGTTGCTCT 287

QY 186 CGTCATCTTCTCCACTCGTGGCGTCTCTATGAGTACGCCCAACACAGTGTGAGGGGTAC 245
Db 288 TGTCATCTTCTCCACTCGAGCGCTCTCTACGAGTACGCCCAACACAGTGTGAGAGGAAC 347

QY 246 AATTGAAAGGTACAGAAAGCTTGTTCGGATGGGTGCGGTCAACCTCTCTCCGTACCCGAAGC 305
Db 348 AATGAAAGGTACAGAAAGCTTGTTCGGATGGGTGCGGTCAACCTCTCTCCGTACCCGAAGC 407

QY 306 TAATACTC--AGTACTATCAGCAAGAGCTCTTAAGCTTCGGAGGAGATTCAGATATT 363
Db 408 TAATACTCAGACTACTATCAGCAAGAGGCGTCTAAACTCCGGAGACAGATTCGGACATT 467

QY 364 CAGAACTCAAATAGGCATATTGTGGGAATCACTTGTGTTCCCT 407
Db 468 CAGAAATTGAACAGACACATCTCTGGTGAATCTCTTGGTTCCCT 511

RESULT 14
AAF85399
ID AAF85399 standard; cDNA; 723 BP.
XX
AC AAF85399;
XX
DT 23-JUL-2001 (first entry)
XX
DE Nucleotide sequence of the floral homeotic protein PTAG-1.
XX
KW Floral homeotic gene; PTD; PTLF; PTAG-1; PTAG-2; floral tissue; LEAFY;
KW LFY; FLORICAULA; FLO; DEFICIENS; DEF; AGAMOUS; AG; transgenic plant;
XX fertility; sterility; ss.
XX
OS Populus balsamifera.
XX
FH Key Location/Qualifiers
FT CDS 1..723
FT /*tag= a
FT /product= "PTAG-1"
XX
PN CA2319853-A1.
XX
PD 01-APR-2001.
XX
PF 02-OCT-2000; 2000CA-2319853.
XX
PR 01-OCT-1999; 99US-0410464.
XX
PA (UYOR-) UNIV OREGON HEALTH SCI.
XX
PI Rottman WH, Strauss SH, Brunner AM, Sheppard LA;
XX WPI; 2001-336098/36.
XX P-PSDB; AAB68437.
XX
PT Novel isolated polynucleotide derived from Populus species, useful for
PT producing transgenic plants having modified fertility characteristic,
PT particularly sterility -
XX
PS Claim 25; Page 55-56; 69pp; English.
XX
CC The present sequence encodes a floral homeotic protein, designated
CC PTAG-1, which is derived from Populus balsamifera subsp. trichocarpa.
CC The specification also describes PTD, PTLF, and PTAG-2 proteins. The
CC floral homeotic proteins are expressed in floral tissues. PTLF is a
CC homologue of LEAFY (LFY) and FLORICAULA (FLO), and is expressed in
CC immature inflorescences on which floral primordia are developing. PTD
CC is a homologue of DEFICIENS (DEF), and is strongly expressed in stamen
CC primordia from the onset of organogenesis. PTAG-1 and PTAG-2 are
CC homologues of AGAMOUS (AG). The floral homeotic proteins and
CC polynucleotides are useful for producing transgenic plants having
CC modified fertility characteristics, particularly sterility.
XX
SQ Sequence 723 BP; 226 A; 147 C; 175 G; 175 T; 0 other;

Query Match 34.1%; Score 305.2; DB 22; Length 723;
Best Local Similarity 73.2%; Pred. No. 2.6e-83;
Matches 391; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

QY 46 AAGAACTAGGGAGGGGAAATAGAGATAAAGAGGATAGAGACACACAAATCGTCAA 105
Db 40 AGGAAGCTGGAGGGGAAAGGTGGAGATCAAGCGGATCGAGAACACCAATCGCCAA 99

QY 106 GTTACTTTCTGCAACGACGCAATGGTCTCTCAAGAAAGCTTATGAATCTCTGTCTTG 165
Db 100 GTCATTTCTGCAAAAGGCGCAGTGGTGTGCTCAAGAAAGCTTATGATTTCTTCTT 159

QY 166 TGTGATGCCGAAGTGGCCCTCGTCATCTCTCTCCACTCGTGGCGCTCTCTATGATACG 225
Db 160 TGGGATGCTGAGGTGCACTCATCGTCTCTCTAGCCGCGGTGCGCTTATGATGATCT 219

QY 226 AACACAGTGTGAGGGGTACAATTGAAAGGTACAGAAAGCTTGTTCGATGCCGTCAAC 285

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Db 220 AACGATAGTCAAAATCAAAATGAGAGGTACAAAAGGCATCTGCAGATTCTTCAAC 279  
QY 286 CCTCCTCCGTCACCGAAGCTAATCTAGTACTAGTACAGCAAGAGCTCTAAGCTTCGG 345  
Db 280 ACTGGGTCTGTTCTGAAGCCAATGCTCAGTACTACCAGCAAGAGCTGCCAAGCTCGGT 339  
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Db 340 TCCCAAAATGGTAATTTGCAGAAATTCAAAACAGGCATATGCTGGGTGAAGCGCTTAGTTCA 399  
QY 406 TTGAACCTTCAAGGAACCTCAAAAACCTAGAAGGAGCTTTGAAAAGGAATCAGCCGTC 465  
Db 400 TTGAGTGTGAAGGAACTTAAGAGTTTGAAGTACGACTTGAGAAAGGAATAAGCAGAATT 459  
QY 466 CGCTCCAAAAGAAATGAGCTGTTAGTGGCAGAGATAGATATATGCAGAAAGGGAATG 525  
Db 460 CGTTCCAAAAGAAATGAGCTGTTGTTGCAGAAATCGAGTATATGCAGAAAGGAGGTT 519  
QY 526 GAGTTGCAACACAATAACATGTACCTGCGAGCAAAAGATAGCCGAAGGCGCCAGA 579  
Db 520 GACTTGCACAACAATAACAGCTTCTCCGAGCAAAAGATTTCAGAGAATGAAAGA 573

RESULT 15  
AAZ57947  
ID AAZ57947 standard; cDNA; 1201 BP.

XX AAZ57947;

XX 11-APR-2000 (first entry)

XX Poplar floral homeotic gene PTAG-1 cDNA.

XX Poplar; PTAG-1; floral homeotic gene; transgenic plant; sterility;  
KW fertility; ss.

XX Populus balsamifera subsp. trichocarpa.

XX Key Location/Qualifiers  
FT 196..921  
FT CDS

FT /\*tag= a  
FT /note= "the coding region is also specifically  
FT claimed in Claim 1"

XX CA2227940-A1.

XX 06-OCT-1999.

XX 07-APR-1998; 98CA-2227940.

XX 06-APR-1998; 98US-0080851.

XX (UYOR-) UNIV OREGON HEALTH SCI.

XX Rottmann WH, Brunner AM, Sheppard LA, Strauss SH;

XX WPI; 2000-106662/10.

XX P-PSDB; AAY58656.

XX Nucleic acid from Populus trichocarpa genes, useful for producing  
PT transgenic plants, particularly trees, with modified fertility  
PT characteristics such as sterility -

XX Claim 1; Page 64-66; 92pp; English.

XX The present sequence is that of cDNA encoding Populus balsamifera  
CC subsp. trichocarpa PTAG-1 protein (see AAY58656). The PTAG-1 gene (see  
CC AAZ57946) is 1 of 4 newly identified floral homeotic genes from this  
CC poplar species. PTAG-1 is a homologue of AGAMOUS and is expressed  
CC in floral tissue. The invention provides nucleic acid sequences of  
CC these 4 Populus genes, the corresponding cDNA sequences (see  
CC AAZ57942-49) and deduced amino acid sequences (see AAY58454-57). It also

CC provides methods of using the genes and cDNA to produce genetically  
CC engineered Populus species and other trees having modified fertility  
CC characteristics, including sterility. Genetic constructs useful in  
CC producing these genetically engineered trees include antisense  
CC versions of PTAG-1, dominant negative mutants, and constructs useful  
CC for sense suppression. Promoter sequences may be used to obtain  
CC floral specific expression of genes such as cytotoxins that may be  
CC used in genetic ablation strategies to produce trees having modified  
CC fertility characteristics, including sterility. Sterile trees  
CC allow increased wood yield and a reduction in the production of  
CC allergens such as pollen.

XX Sequence 1201 BP; 354 A; 251 C; 257 G; 339 T; 0 other;

QY Query Match 34.1%; Score 305.2; DB 21; Length 1201;

Db Best Local Similarity 73.2%; Pred. No. 3.3e-83;

QY Matches 391; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

QY 46 AAGAACTAGGAGAGGAGAAATAGAGATAAGAGGATAGAGAACACAAATCGTCAA 105

Db 235 AGGAAGCTGGGAAGGGAAAGGTGGAGATCAAGCGGATCGAGAACACCAATCGCCAA 294

QY 106 GTTACTTTCTGCAACGACGCAATGGTCTTCTCAAGAAAGCTTATGAACCTCTCTGTTG 165

Db 295 GTCACTTTCTGCAAAAGGCGCAGTGGTTGCTCAAGAAAGCCTACGAATTATCTGTTCT 354

QY 166 TGTGATGCCGAAGTTGCCCTCGTCATCTTCTCCACTCGTGGCGTCTCTATAGTAGGCC 225

Db 355 TGCATGCTGAGGTGCACTCATCTCTCTAGCCGCGTCCCTTATGAGTACTCT 414

QY 226 AACACAGTGTGAGGGGTACAATGAAAGGTACAAGAGCTTGTTCGATGCCGTCAAC 285

Db 415 AACGATAGTGTCAAAATCAACAATTGAGAGGTACAAGAGGCATCTGCAGATTCTTCAAC 474

QY 286 CTTCTTCCGTCACCGAAGCTAATCTACTAGTACTATATCAGCAAGAGCCTTAAAGCTTCGG 345

Db 475 ACTGGTCTGTTTCTGAAGCCCAATGCTCAGTACTACCAGCAAGAGCTGCCAGCTGCGT 534

QY 346 AGGAGATTCCGAGATATTTCAGAAATTCAGATAGGCATATGTTGGGGAATCAGTTGGTTCC 405

Db 535 TCCCAAAATGGTAATTTGCAGAAATTCAAACAGGCATATGCTGGGTGAAGCGCTTAGTTCA 594

QY 406 TTGAACCTTCAAGGAACCTCAAAAACCTAGAGGAGCTTGTGAAAAGGAATCAGCCGTC 465

Db 595 TTGAGTGTGAAGGAACTTAAGAGTTTGGAAATACGACTTGAGAAAGGAATAAGCAGAATT 654

QY 466 CGTCCAAAAGAAATGAGCTGTTAGTGGCAGAGATAGATATATGCAGAAAGGGAATG 525

Db 655 CGTTCCAAAAGAAATGAGCTGTTGTTGGCAGAAATCGAGTATATGCAGAAAGGAGGTT 714

QY 526 GAGTTGCAACACAATAACATGTACTGCGAGCAAAAGATAGCCGAAGGCGCCAGA 579

Db 715 GACTTGCACAACAATAACAGCTTCTCCGAGCAAAAGATTTCAGAGAATGAAAGA 768

Search completed: February 2, 2003, 08:18:57  
Job time : 243.706 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run'on: February 2, 2003, 08:19:29 ; Search time 2453.74 Seconds  
(without alignments)  
10627.107 Million cell updates/sec

Title: US-09-978-382A-3  
Perfect score: 896  
Sequence: 1 ggataatggaggaggtgg.....actgtgtttttttgttca 896

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*

- 1: gb\_ba:\*
- 2: gb\_htg:\*
- 3: gb\_in:\*
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- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_pl:\*
- 9: gb\_pr:\*
- 10: gb\_ro:\*
- 11: gb\_sts:\*
- 12: gb\_sy:\*
- 13: gb\_un:\*
- 14: gb\_vi:\*
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- 17: em\_hum:\*
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- 33: em\_htg\_mus:\*
- 34: em\_htg\_pln:\*
- 35: em\_htg\_rod:\*
- 36: em\_htg\_mam:\*
- 37: em\_htg\_vrt:\*
- 38: em\_sy:\*
- 39: em\_htgo\_hum:\*
- 40: em\_htgo\_mus:\*
- 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query Match % | Score | Length | DB | ID        | Description        |
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| 2          | 895           | 99.9  | 895    | 8  | ATHAGL1A  | M55550 Arabidopsis |
| 3          | 887           | 99.0  | 1202   | 8  | AY086196  | AY086196 Arabidops |
| 4          | 634.4         | 70.8  | 789    | 8  | AY036062  | AY036062 Brassica  |
| 5          | 536.8         | 59.9  | 959    | 6  | ARI38348  | ARI38348 Sequence  |
| 6          | 536.8         | 59.9  | 963    | 8  | ATHAGL5A  | M55553 Arabidopsis |
| 7          | 344.8         | 38.5  | 1125   | 6  | AR003863  | AR003863 Sequence  |
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| 9          | 343.2         | 38.3  | 1084   | 8  | TOMTAG1A  | L26295 Lycopersico |
| 10         | 335.8         | 37.5  | 5622   | 6  | ARI38345  | ARI38345 Sequence  |
| 11         | 335.8         | 37.5  | 5622   | 6  | AX320929  | AX320929 Sequence  |
| 12         | 334.2         | 37.3  | 90273  | 8  | ATT20N10  | AL353032 Arabidops |
| 13         | 333.6         | 37.2  | 1065   | 8  | MDO251117 | AJ251117 Malus dom |
| 14         | 325.6         | 36.3  | 1214   | 8  | PHPMADS3  | X72912 P.hybrida p |
| 15         | 319.8         | 35.7  | 1160   | 8  | AF265562  | AF265562 Vitis vin |
| 16         | 319.2         | 35.6  | 1065   | 8  | AB025643  | AB025643 Rosa rugo |
| 17         | 318           | 35.5  | 1224   | 8  | PETFHP    | L33973 Petunia inf |
| 18         | 316.4         | 35.3  | 956    | 8  | PHFBP6A   | X68675 P.hybrida f |
| 19         | 313.4         | 35.0  | 1080   | 8  | PGORFGAG2 | S46612 P.ginseng g |
| 20         | 305.4         | 34.1  | 1073   | 8  | S53900    | S53900 ple-plena l |
| 21         | 297.2         | 33.2  | 1197   | 8  | AF103903  | AF103903 Liquidamb |
| 22         | 295.6         | 33.0  | 1082   | 8  | AF265554  | AF265554 Cucumis s |
| 23         | 294.8         | 32.9  | 1165   | 8  | BPE252071 | AJ252071 Betula pe |
| 24         | 292.8         | 32.7  | 1128   | 8  | DCA271150 | AJ271150 Daucus ca |
| 25         | 292.6         | 32.7  | 967    | 8  | CSCUS1    | X97801 C.sativus C |
| 26         | 292.4         | 32.6  | 1179   | 8  | AF027376  | AF027376 Corylus a |
| 27         | 291           | 32.5  | 1000   | 8  | AF022378  | AF022378 Cucumis s |
| 28         | 290.8         | 32.5  | 1157   | 6  | AX006357  | AX006357 Sequence  |
| 29         | 290.8         | 32.5  | 1158   | 8  | AF035438  | AF035438 Cucumis s |
| 30         | 290.8         | 32.5  | 1160   | 8  | AF022379  | AF022379 Cucumis s |
| 31         | 290.6         | 32.4  | 1037   | 8  | MDO251118 | AJ251118 Malus dom |
| 32         | 289.8         | 32.3  | 1142   | 8  | AF022377  | AF022377 Cucumis s |
| 33         | 286.6         | 32.0  | 1009   | 8  | AF234617  | AF234617 Phalaenop |
| 34         | 284.4         | 31.7  | 1097   | 6  | AR003862  | AR003862 Sequence  |
| 35         | 284.4         | 31.7  | 1098   | 8  | BNABAG1X  | M99415 Brassica na |
| 36         | 284.4         | 31.7  | 1345   | 8  | CSA312773 | AJ312773 Cucumis s |
| 37         | 283.8         | 31.7  | 763    | 8  | AY083173  | AY083173 Gossypium |
| 38         | 282.4         | 31.5  | 905    | 8  | ATU20182  | U20182 Arabidopsis |
| 39         | 282.4         | 31.5  | 1057   | 8  | AY087201  | AY087201 Arabidops |
| 40         | 278.2         | 31.0  | 1054   | 8  | AB025644  | AB025644 Rosa rugo |
| 41         | 278.2         | 31.0  | 1116   | 8  | RH043372  | U43372 Rosa hybrid |
| 42         | 277.8         | 31.0  | 1073   | 8  | AB025646  | AB025646 Rosa rugo |
| 43         | 276.4         | 30.8  | 977    | 8  | AF286649  | AF286649 Cucumis s |
| 44         | 275.8         | 30.8  | 1457   | 6  | AR003861  | AR003861 Sequence  |
| 45         | 275.8         | 30.8  | 1458   | 8  | ATAGAMSG  | X53579 A.thaliana  |

ALIGNMENTS

|            |            |                                                     |        |     |        |                 |
|------------|------------|-----------------------------------------------------|--------|-----|--------|-----------------|
| RESULT 1   | ARI38347   | Sequence 5 from patent US 6198024.                  | 896 bp | DNA | linear | PAT 16-JUN-2001 |
| LOCUS      | ARI38347   | Sequence 5 from patent US 6198024.                  |        |     |        |                 |
| DEFINITION | ARI38347   | Sequence 5 from patent US 6198024.                  |        |     |        |                 |
| ACCESSION  | ARI38347   | Sequence 5 from patent US 6198024.                  |        |     |        |                 |
| VERSION    | ARI38347.1 | GI:14479856                                         |        |     |        |                 |
| KEYWORDS   |            |                                                     |        |     |        |                 |
| SOURCE     |            | Unknown.                                            |        |     |        |                 |
| ORGANISM   |            | Unknown.                                            |        |     |        |                 |
| REFERENCE  |            | Unclassified.                                       |        |     |        |                 |
| AUTHORS    |            | 1 (bases 1 to 896)                                  |        |     |        |                 |
| TITLE      |            | Yanofsky,M.F. and Ferrandiz,C.                      |        |     |        |                 |
| JOURNAL    |            | Seed plants characterized by delayed seed dispersal |        |     |        |                 |
| FEATURES   |            | Patent: US 6198024-A 5 06-MAR-2001;                 |        |     |        |                 |
|            |            | Location/Qualifiers                                 |        |     |        |                 |

|                           |     |                                                               |     |  |  |  |  |  |  |  |  |
|---------------------------|-----|---------------------------------------------------------------|-----|--|--|--|--|--|--|--|--|
| source                    |     | 1. .896                                                       |     |  |  |  |  |  |  |  |  |
| BASE COUNT                |     | 285 a 186 c 205 g 220 t                                       |     |  |  |  |  |  |  |  |  |
| ORIGIN                    |     |                                                               |     |  |  |  |  |  |  |  |  |
| Query Match               |     | 100.0%; Score 896; DB 6; Length 896;                          |     |  |  |  |  |  |  |  |  |
| Best Local Similarity     |     | 100.0%; Pred. No. 5.5e-236;                                   |     |  |  |  |  |  |  |  |  |
| Matches 896; Conservative |     | 0; Mismatches 0; Indels 0; Gaps 0;                            |     |  |  |  |  |  |  |  |  |
| Qy                        | 1   | GGATCAATGGAGGAAGGTGGGAGTAGTACGACGACGAGAGTAGCAAGAACTAGGGAGA    | 60  |  |  |  |  |  |  |  |  |
| Db                        | 1   | GGATCAATGGAGGAAGGTGGGAGTAGTACGACGACGAGAGTAGCAAGAACTAGGGAGA    | 60  |  |  |  |  |  |  |  |  |
| Qy                        | 61  | GGGAAATAGAGATAAAGAGGATAGAGAAACACAAATCGTCAAGTTACTTTCTGCAAA     | 120 |  |  |  |  |  |  |  |  |
| Db                        | 61  | GGGAAATAGAGATAAAGAGGATAGAGAAACACAAATCGTCAAGTTACTTTCTGCAAA     | 120 |  |  |  |  |  |  |  |  |
| Qy                        | 121 | CGACGCAATGGTCTTCTCAAGAAAGCTTATCAACTCTCTGTGTGTGTCATGCCGAAGTT   | 180 |  |  |  |  |  |  |  |  |
| Db                        | 121 | CGACGCAATGGTCTTCTCAAGAAAGCTTATCAACTCTCTGTGTGTGTCATGCCGAAGTT   | 180 |  |  |  |  |  |  |  |  |
| Qy                        | 181 | GCCCTCGTCATCTTCTCCACTCGTGCCCGTCTCTATGAGTACGCCCAACACAGTGTGAGG  | 240 |  |  |  |  |  |  |  |  |
| Db                        | 181 | GCCCTCGTCATCTTCTCCACTCGTGCCCGTCTCTATGAGTACGCCCAACACAGTGTGAGG  | 240 |  |  |  |  |  |  |  |  |
| Qy                        | 241 | GGTACAATTGAAAGGTACAGAAAGCTTGTTCGGATGCCGTCACCCCTCTCCGTCACC     | 300 |  |  |  |  |  |  |  |  |
| Db                        | 241 | GGTACAATTGAAAGGTACAGAAAGCTTGTTCGGATGCCGTCACCCCTCTCCGTCACC     | 300 |  |  |  |  |  |  |  |  |
| Qy                        | 301 | GAAGCTAATCTCAGTACTATCAGCAAGAGCCTCTAAGCTTCGGAGCGAGATTCGAGAT    | 360 |  |  |  |  |  |  |  |  |
| Db                        | 301 | GAAGCTAATCTCAGTACTATCAGCAAGAGCCTCTAAGCTTCGGAGCGAGATTCGAGAT    | 360 |  |  |  |  |  |  |  |  |
| Qy                        | 361 | ATTCAGAATTCAAAATAGGCATATTGTTGGGAATCACTTGGTTCCTTGAACCTTCAAGGAA | 420 |  |  |  |  |  |  |  |  |
| Db                        | 361 | ATTCAGAATTCAAAATAGGCATATTGTTGGGAATCACTTGGTTCCTTGAACCTTCAAGGAA | 420 |  |  |  |  |  |  |  |  |
| Qy                        | 421 | CTCAAAAACCTAGAAGGACGCTTGAAGAAAGCAATCAGCCCGTGTCCGCTCCAAAAAGAA  | 480 |  |  |  |  |  |  |  |  |
| Db                        | 421 | CTCAAAAACCTAGAAGGACGCTTGAAGAAAGCAATCAGCCCGTGTCCGCTCCAAAAAGAA  | 480 |  |  |  |  |  |  |  |  |
| Qy                        | 481 | GAGCTGTAGTGGCAGAGATAGAGTATATGCAGAGAGGGAATGGAGTTGCAACACAA      | 540 |  |  |  |  |  |  |  |  |
| Db                        | 481 | GAGCTGTAGTGGCAGAGATAGAGTATATGCAGAGAGGGAATGGAGTTGCAACACAA      | 540 |  |  |  |  |  |  |  |  |
| Qy                        | 541 | AACATGTACCTCGGAGCAAAAGATAGCCGAAGGCCAGATTGAATCCGGACCCAGCAGAA   | 600 |  |  |  |  |  |  |  |  |
| Db                        | 541 | AACATGTACCTCGGAGCAAAAGATAGCCGAAGGCCAGATTGAATCCGGACCCAGCAGAA   | 600 |  |  |  |  |  |  |  |  |
| Qy                        | 601 | TCGAGTGTGATACAAAGGACGACAGTTTACGAATCCGGTGTATCTTCTCATGACCATCG   | 660 |  |  |  |  |  |  |  |  |
| Db                        | 601 | TCGAGTGTGATACAAAGGACGACAGTTTACGAATCCGGTGTATCTTCTCATGACCATCG   | 660 |  |  |  |  |  |  |  |  |
| Qy                        | 661 | CAGCATATATAATCGGAACCTATATTCGGGTGAACCTTCTTGAACCGGAATCAGCAATTC  | 720 |  |  |  |  |  |  |  |  |
| Db                        | 661 | CAGCATATATAATCGGAACCTATATTCGGGTGAACCTTCTTGAACCGGAATCAGCAATTC  | 720 |  |  |  |  |  |  |  |  |
| Qy                        | 721 | GGCCAAGACCAACCTCCTCTCAACTGTGTGAACCTCAAAACATGATAACTGTTTCTTCC   | 780 |  |  |  |  |  |  |  |  |
| Db                        | 721 | GGCCAAGACCAACCTCCTCTCAACTGTGTGAACCTCAAAACATGATAACTGTTTCTTCC   | 780 |  |  |  |  |  |  |  |  |
| Qy                        | 781 | CCTCATAACGATTAAAGAGAGACGAGAGAGTTTCATTTTATATTATTAACCGCACTGTGT  | 840 |  |  |  |  |  |  |  |  |
| Db                        | 781 | CCTCATAACGATTAAAGAGAGACGAGAGAGTTTCATTTTATATTATTAACCGCACTGTGT  | 840 |  |  |  |  |  |  |  |  |
| Qy                        | 841 | ATTCATAGTTTAGGTTCTAATAATGATAATAACAAAACCTGTTGTTTCTTCTGCTTCA    | 896 |  |  |  |  |  |  |  |  |
| Db                        | 841 | ATTCATAGTTTAGGTTCTAATAATGATAATAACAAAACCTGTTGTTTCTTCTGCTTCA    | 896 |  |  |  |  |  |  |  |  |

RESULT 2

ATHAGLLA

LQCUS

ATHAGLLA 895 bp mRNA linear PLN 27-APR-1993

DEFINITION Arabidopsis thaliana transcription factor (AGL1), complete cds.  
ACCESSION M55550  
VERSION M55550.1 GI:166587  
KEYWORDS transcription factor.  
SOURCE Arabidopsis thaliana (strain Landsberg erecta) flower cDNA to mRNA.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi

REFERENCE 1 (bases 1 to 895)  
AUTHORS Ma,H., Yanofsky,M.F. and Meyerowitz,E.M.  
TITLE AGL1-AGL6, an Arabidopsis gene family with similarity to floral homeotic and transcription factor genes  
JOURNAL Genes Dev. 5 (3), 484-495 (1991)  
MEDLINE 91160981  
PUBMED 1672119

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BASE COUNT  
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Best Local Similarity 100.0%; Pred. No. 1e-235;  
Matches 895; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATCAATGAGGAGGAGTGGGAGTAGTACGACGACGAGAGTAGCAAGAACTAGGGAGA 60  
Db 1 GGATCAATGAGGAGGAGTGGGAGTAGTACGACGACGAGAGTAGCAAGAACTAGGGAGA 60  
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Db 61 GGGAAATAGAGATAAAGAGGATAGAGAACACACAAATCGTCAAGTTACTTTCTGCAAA 120

QY 121 CGACGCAATGGTCTTCTCAAGAAAGCTTATGAACCTCTCTGTCTTGTGTGATGCCGAAGTT 180  
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QY 181 GCCTCTGTCATCTTCTCCACTCGTGGCGTCTCTATGAGTACGCCAACACAGTGTGAGG 240  
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DEFINITION Arabidopsis thaliana clone 22339 mRNA, complete sequence.  
ACCESSION AY086196  
VERSION AY086196.1 GI:21404906  
KEYWORDS FLI\_CDNA.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 1202)  
Haas,B.J., Volfovsky,N., Town,C.D., Troupkan,M., Alexandrov,N.,  
Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.  
Full-length messenger RNA sequences greatly improve genome  
annotation  
TITLE Genome Biol. (2002) In press  
JOURNAL  
REFERENCE 2 (bases 1 to 1202)  
AUTHORS Brover,V., Troupkan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and

TITLE Full-length cDNA from Arabidopsis thaliana  
JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 1202)  
AUTHORS Brover,V., Troupkan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and  
Feldmann,K.  
TITLE Direct Submission  
JOURNAL Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,  
Malibu, CA 90265, USA  
COMMENT This clone sequence is one of 5,000 Ceres full-length cDNAs made  
available to TIGR and Genbank. The following quality assessment of  
this set was done by comparison with known proteins: two percent of  
the clones are estimated to be 5'-truncated; less than one percent  
are 3'-truncated; approximately two percent represent alternative  
splice variants, including unspliced introns and spliced exons; one  
percent may contain premature stop codons; five percent may have  
frame shifts in a coding region. A sequence is considered to be  
5'-truncated if it lacks the translation initiation start (ATG). A  
sequence is considered to be 3'-truncated if it lacks the  
C-terminal end of the encoded protein. Please note that these cDNA  
sequences are derived from the Ws or Laer ecotypes and therefore  
may contain polymorphisms when compared to sequences from Col-0.  
Genset carried out the library production and sequencing of the  
full-length clones. Ceres, Inc. carried out the clustering of the  
5' sequences, selection of clones, and sequence assembly.  
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Best Local Similarity 100.0%; Pred. No. 1.7e-233;  
Matches 887; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 316 GGATCAATGGAGGAGGTGGGAGTAGTCAGCAGCAGAGAGTAGCAAGAACTAGGGAGA 375  
QY 61 GGGAAAAATAGAGATAAAGAGGATAGAGAGACACACAAATCGTCAAGTTACTTTCTGCAA 120  
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QY 361 ATTCAGAAATTCAGATAGGATATTGTTGGGGAATCATTGGTTCCTTGAACCTCAAGGAA 420

Db 676 ATTCAGAAATCAAAATAGGCATATTTGTTGGGAATCACTTGGTTCCTTGAACCTCAAGGAA 735

QY 421 CTCAAAAACCTAGAGGAGCTCTTGAAAAAGGAATCAGCGGTGTCGGTCCAAAGAAAT 480

Db 736 CTCAAAAACCTAGAGGAGCTCTTGAAAAAGGAATCAGCGGTGTCGGTCCAAAGAAAT 795

QY 481 GAGCTGTTAGTGGCAGAGATAGATATATGTCAGAGAGGAGGAAATGGAGTTGCAACACAAT 540

Db 796 GAGCTGTTAGTGGCAGAGATAGATATATGTCAGAGAGGAGGAAATGGAGTTGCAACACAAT 855

QY 541 AACATGTACCTCGAGCAAGATAGCCGAGGCGCCAGATTGAATCCGGACCCAGCAGGAA 600

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Db 1156 ATTCATAGTTAGTTCTAATAATGATAATAACAAAACCTGTGTTTC 1202

RESULT 4

AY036062

LOCUS

Brassica napus SHATTERPROOF1 (BnSHP1) mRNA, complete cds.

AY036062

AY036062.1 GI:17223669

Brassica napus.

Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 789)

PyLauik,J.D., Davis,A.R. and Bonham-Smith,P.C.

Isolation of the coding region of BnSHP by RT-PCR

Unpublished

2 (bases 1 to 789)

PyLauik,J.D., Davis,A.R. and Bonham-Smith,P.C.

Direct Submission

Submitted (17-MAY-2001) Biology, University of Saskatchewan, 112 Science Place, Saskatoon, SK S7N 5E2, Canada

Location/Qualifiers

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/organism="Brassica napus"

/db\_xref="taxon:3708"

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/gene="BnSHP1"

/note="genomic sequence found in GenBank Accession Number AF226865"

1. .39

/gene="BnSHP1"

40. .789

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/note="putative transcription factor"

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/product="SHATTERPROOF1"

/protein\_id="AAK62033.1"

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FEATURES

source

gene

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SQHYNRNYPVNLLEPNQOFSQDQPPQLV"

BASE COUNT 245 a 159 c 193 g 192 t

ORIGIN

Query Match 70.8%; Score 634.4; DB 8; Length 789;  
Best Local Similarity 90.9%; Pred. No. 7.2e-164;  
Matches 687; Conservative 0; Mismatches 66; Indels 3; Gaps 1;

QY 1 GGATCAATCGAGGAAGTGGGAGTAGTACAGCGCAGAGAGTAGCAAGAACTAGGGAGA 60

Db 34 GAACCAATGGATGAAGTGGGAGTAGTACAGCGCAGAGAGTAGCAAGAACTAGGGAGA 93

QY 61 GGGAAAAATAGAGATAAAGAGGATAGAGAACACAAATCGTCAAGTTACTTCTGCAA 120

Db 94 GGGAGATAGAGATAAAGAGGATAGAGAACACAAATCGTCAAGTTACTTCTGCAA 153

QY 121 CGAGCAATGGTCTTCTCAAGAAAGCTTATGACTCTCTGTCTTGTGTGATGCCGAAGTT 180

Db 154 CGAGCAATGGTCTTCTCAAGAAAGCTTATGAGCTCTCTGTCTTGTGTGATGCCGAAGTT 213

QY 181 GCCCTCGTCATCTTCTCCACTCGTGGCGCTCTCTATGAGTACGCCAACACAGTGTGAGG 240

Db 214 GCCCTCGTATCTTCTCCACTCGTGGCGCTTCTTATGAGTACGCCAACACAGTGTGAGG 273

QY 241 GGTACAATGAAAGGTACAGAAAGCTTGTCCGATGCCGTCAACCCCTCTTCCGTACC 300

Db 274 GGTACAATGAAAGGTACAGAAAGCTTGTCCGATGCCGTCAACCCCTCTTACTGTCACT 333

QY 301 GAAGTAACTACTAGTACTATCAGCAAGAGCCCTTAAGCTTCGGAGGAGATTCGAGAT 360

Db 334 GAAGTAACTACTAGTACTATCAGCAAGAGCCCTTAAGCTTCGGAGGAGATTCGAGGAC 393

QY 361 ATTCAGAAATCAAAATAGGCATATTTGTTGGGAATCACTTGGTTCCTTGAACCTCAAGGAA 420

Db 394 ATTCAGAAATCGAACAGGCAATATTTGTTGGGAATCACTTGGTTCCTTGAACCTCAAGGAA 453

QY 421 CTCAAAAACCTAGAGGAGCTCTTGAAAAAGGAATCAGCGGTGTCGGTCCCAAAAAGAAAT 480

Db 454 CTCAAAAACCTAGAGGAGCTCTTGAAAAAGGAATCAGCGGTGTCGGTCCCAAAAAGAAAT 513

QY 481 GAGCTGTTAGTGGCAGAGATAGATATATGTCAGAGAGGAGGAAATGGAGTTGCAACACAAT 540

Db 514 GAACTTTAGTGGCAGAGATAGATATATGTCAGAGAGGAGGAAATGGAGTTGCAACACAAT 573

QY 541 AACATGTACCTCGAGCAAGATAGCCGAGGCGCCAGATTGAATCCGGACCCAGCAGGAA 600

Db 574 AACATGTACCTCGAGCAAGATAGCCGAGGCGCCAGATTGAATCCGGACCCAGCAGGAA 633

QY 601 TCGAGTGTGATACAGGGAGCAGACTTTACGAATCCGGTGT---ATCTTCTCATGACCAG 657

Db 634 TCCGGTGTATACAGGGAGCGCGGTATTATGAGTCCGGTCTGTCTTCTTCTCATGATCAG 693

QY 658 TCGCAGCATTAATAATCGGAATATATTCGGTGAACCTCTTGAACCGCAATCAGCAATTC 717

Db 694 TCGCAGCATTAATAATCGGAATATATTCGGTGAACCTCTTGAACCGCAATCAGCAATTC 753

QY 718 TCCGGCCCAAGACCAACCTCTCTTCAACTTGTGTA 753

Db 754 TCCGGTCAAGACCAACCTCTCTTCAACTTGTGTA 789

RESULT 5

AR138348

LOCUS

DEFINITION Sequence 7 from patent US 6198024.

ACCESSION AR138348

VERSION AR138348.1 GI:14479857

KEYWORDS

SOURCE

Unknown.

linear PAT 16-JUN-2001











Db 531 CGATCCAAAAGAAATGACGTGTTCTTTGCTGAAATGAGTATATGCGAAGAGGGAACTT 590

Qy 526 GAGTTGCAACACATAACATGTACCTGCGAGCAAGATAGCCGAAGGCCGACAGATTGAAT 585

Db 591 GATTTACACAACAACAATCAGTACCTGAGAGCAAGAAATGCTGAAACTGAGAGAGCTCAG 650

Qy 586 CCGGACGAGCAGGAATCGAGTGTGATACAAAGGAGCAGACAGTTACGAATCCGGTGTATCT 645

Db 651 CATCAGCATCAGCAGATGAATCTGATCCAGGAGTTTCATCAAACTATCATGAGCTTGTG 710

Qy 646 TCTCATGACGAGTCCGAGCATTATAATCGAACTATATTCGGGTGAACCTTCTGTGAACCG 705

Db 711 CCTCCACCTCA--GCAATTCGATACTCGAACTATCTACAAAGTAAATGAGTTGCAACACC 767

Qy 706 AATCAGCAATTCCTCGGCCAAGACCAACCTCCTCTTCAACTTGTGTAA 753

Db 768 AACACCATTAACCTAGACAAAGACCAACCCCTATTCAACTAGTCTAA 815

RESULT 10

AR138345

LOCUS AR138345 5622 bp DNA linear PAT 16-JUN-2001

DEFINITION Sequence 3 from patent US 6198024.

ACCESSION AR138345

VERSION AR138345.1 GI:14479854

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 5622)

AUTHORS Yanofsky,M.F. and Ferrandiz,C.

TITLE Seed plants characterized by delayed seed dispersal

JOURNAL Patent: US 6198024-A 3 06-MAR-2001;

FEATURES Location/Qualifiers

source

BASE COUNT 1853 a 928 c 907 g 1927 t 7 others

ORIGIN

Query Match 37.5%; Score 335.8; DB 6; Length 5622;

Best Local Similarity 99.4%; Pred. No. 1.8e-81;

Matches 337; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 558 AAAGATAGCCGAAGGCCAGATTGAATCCGGACCAGCAGGAATCGAGTGTGATACAAGG 617

Db 5025 ATAGATAGCCGAAGGCCAGATTGAATCCGGACCAGCAGGAATCGAGTGTGATACAAGG 5084

Qy 618 GACGACAGTTTACGAATCCGGTGTATCTTCATGACCACTCGCAGCATTTATAATCGGAA 677

Db 5085 GACGACAGTTTACGAATCCGGTGTATCTTCATGACCACTCGCAGCATTTATAATCGGAA 5144

Qy 678 CTATATTCGGTGAACCTTCTTGAACCGAATCAGCAATCTCCGGCCCAAGACCAACCTCC 737

Db 5145 CTATATTCGGTGAACCTTCTTGAACCGAATCAGCAATCTCCGGCCCAAGACCAACCTCC 5204

Qy 738 TCTTCAACTTGTGTAACCTCAAAACATGATACTTCTTCCCTCATACGATTAAAGA 797

Db 5205 TCTTCAACTTGTGTAACCTCAAAACATGATACTTCTTCCCTCATACGATTAAAGA 5264

Qy 798 GAGAGCAGGAGAGTTCATTTATATTTATAACGCGACTGTGTATTCATAGTTAGGTTTC 857

Db 5265 GAGAGCAGGAGAGTTCATTTATATTTATAACGCGACTGTGTATTCATAGTTAGGTTTC 5324

Qy 858 TAATAATGATAATAACAAACTGTTGTTCTTCTTCTTCTTCA 896

Db 5325 TAATAATGATAATAACAAACTGTTGTTCTTCTTCTTCTTAA 5363

RESULT 11

AX320929

LOCUS AX320929 5622 bp DNA linear PAT 14-DEC-2001

DEFINITION Sequence 5 from Patent WO0179517.

ACCESSION AX320929

AX320929.1 GI:17902476

thale cress.

Arabidopsis thaliana

REFERENCE 1 Liljegren,S. and Yanofsky,M.F.

AUTHORS Control of fruit dehiscence in arabidopsis by indehiscen1 genes

TITLE Patent: WO 0179517-A 5 25-OCT-2001;

JOURNAL The Regents of the University of California (US)

FEATURES Location/Qualifiers

source

I. .5622

/organism="Arabidopsis thaliana"

/db\_xref="taxon:3702"

/note="SHATTERPROOF1 (SHPL) genomic"

BASE COUNT 1853 a 928 c 907 g 1927 t 7 others

ORIGIN

Query Match 37.5%; Score 335.8; DB 6; Length 5622;

Best Local Similarity 99.4%; Pred. No. 1.8e-81;

Matches 337; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 558 AAAGATAGCCGAAGGCCAGATTGAATCCGGACCAGCAGGAATCGAGTGTGATACAAGG 617

Db 5025 ATAGATAGCCGAAGGCCAGATTGAATCCGGACCAGCAGGAATCGAGTGTGATACAAGG 5084

Qy 618 GACGACAGTTTACGAATCCGGTGTATCTTCATGACCACTCGCAGCATTTATAATCGGAA 677

Db 5085 GACGACAGTTTACGAATCCGGTGTATCTTCATGACCACTCGCAGCATTTATAATCGGAA 5144

Qy 678 CTATATTCGGTGAACCTTCTTGAACCGAATCAGCAATCTCCGGCCCAAGACCAACCTCC 737

Db 5145 CTATATTCGGTGAACCTTCTTGAACCGAATCAGCAATCTCCGGCCCAAGACCAACCTCC 5204

Qy 738 TCTTCAACTTGTGTAACCTCAAAACATGATACTTCTTCCCTCATACGATTAAAGA 797

Db 5205 TCTTCAACTTGTGTAACCTCAAAACATGATACTTCTTCCCTCATACGATTAAAGA 5264

Qy 798 GAGAGCAGGAGAGTTCATTTATATTTATAACGCGACTGTGTATTCATAGTTAGGTTTC 857

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Qy 858 TAATAATGATAATAACAAACTGTTGTTCTTCTTCTTCTTCA 896

Db 5325 TAATAATGATAATAACAAACTGTTGTTCTTCTTCTTCTTAA 5363

RESULT 12

ATT20N10

LOCUS Arabidopsis thaliana DNA linear PLN 19-APR-2000

DEFINITION Arabidopsis thaliana DNA chromosome 3, BAC clone r20N10.

ACCESSION AL353032

VERSION AL353032.1 GI:7630060

KEYWORDS Arabidopsis thaliana.

SOURCE Arabidopsis thaliana

ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 90273)

AUTHORS D'Angelo,M., Vezzi,A., Modesto,D., Pigazzi,M., Valle,G., Mewes,H.W., Rudd,S., Lemcke,K., Mayer,K.F.X., Quetier,F. and Salanoubat,M.

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 90273)

AUTHORS EU Arabidopsis sequencing,project.

TITLE Direct Submission

JOURNAL Submitted (19-APR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project Coordinator: Marcel Salanoubat and Francis Quetier, Groupement

d'Interet Public, Centre National de Sequencage - GENOSCOPE; 2 rue Gaston Cremieux, BP191, 91006 Evry Cedex, France;  
http://www.genoscope.cns.fr  
Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.  
Location/Qualifiers

FEATURES  
source

1. .90273  
/organism="Arabidopsis thaliana"  
/variety="Columbia"  
/db\_xref="taxon:3702"  
/chromosome="3"

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/gene="T20N10\_10"

CDS 1429. .2769

/gene="T20N10\_10"  
/note="similarity to PKI protein, Homo sapiens,  
EMBL: HSA7398"  
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/product="putative protein"  
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LPRVIGKFFTKKIPVALDLKRNWRKHQIEKACGSAMFFIRGTCSVIKVGKLSMDI  
CEITENYMATLNGLEFPLPNKWTYVRSILHLKLSLALPIYOSVPLDKLIKIDAFGSGK  
SVVOEKEGEVEVAVDGGKSVTGKGGKKGRHVEVRYMSNVAEVLDEDEIGGDE  
DNNEIVESEKKMKRKEVSEVAESEKPMKKAAGKLPDVEKPMKKAAGKSKPDV  
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exon

gene 3548. .5169  
/number=1

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CDS

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/note="similarity to predicted protein, Arabidopsis  
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/translation="MPYFIQRLFNTCKSSLPNGPVSEALDKVRNVLEKIPKSDVGL  
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intron

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exon

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EMBL: AB002282"

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7222. .7363  
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7364. .7797  
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7798. .7881  
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exon

number=2

7882. .8190  
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intron

number=2

8191. .8273  
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exon

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8274. .8360  
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intron

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8361. .8480  
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CDS

/note="similarity to serine/threonine-specific protein  
kinase NAK, Arabidopsis thaliana, PIR:S38326  
Contains Prokaryotic membrane lipoprotein lipid attachment  
site AA13-23;Protein kinases signatures and profile  
AA79-101;Protein kinases signatures and profile AA198-210"

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number=2

9800. .9914  
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intron

exon /number=2  
9915..10050  
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10510..10606  
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10607..10739  
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intron /number=5  
10740..10819  
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/note="strong similarity to ribosomal protein L11,  
cytosolic, Arabidopsis thaliana, PIR:S49033  
Contains Ribosomal protein L5 signature AA39-55"  
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/product="ribosomal protein L11-like"

Query Match 37.3%; Score 334.2; DB 8; Length 90273;  
Best Local Similarity 99.1%; Pred. No. 6e-81;  
Matches 336; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 558 AAGATAGCCGAAGGCCGACGATTGAATCCGGACGACGAGCAATCGAGTGTGATACAAGG 617  
Db 41426 ATAGATAGCCGAAGGCCGACGATTGAATCCGGACGACGAGCAATCGAGTGTGATACAAGG 41485  
QY 618 GACGACAGTTTACGAATCCGGTGTATCTTCTCATGACCACTCGCAGCATTAATACGGAA 677  
Db 41486 GACGACAGTTTACGAATCCGGTGTATCTTCTCATGACCACTCGCAGCATTAATACGGAA 41545  
QY 678 CTATATTCGGGTGAACCTTCTGAACCGGAATCAGCAATCTCCGGCCCAAGCAACCTCC 737  
Db 41546 CTATATTCGGGTGAACCTTCTGAACCGGAATCAGCAATCTCCGGCCCAAGCAACCTCC 41605  
QY 738 TCTTCACTTGTGTAACCTCAAAACATGATACTTGTCTTCTCCCTCATACGATTAAAGA 797  
Db 41606 TCTTCACTTGTGTAACCTCAAAACATGATACTTGTCTTCTCCCTCATACGATTAAAGA 41665  
QY 798 GAGAGCAGAGAGTTCATTTTATATTATTAACGCGACTGTGTAATCATAGTTTAGGTTTC 857  
Db 41666 GAGAGCAGAGAGTTCATTTTATATTATTAACGCGACTGTGTAATCATAGTTTAGGTTTC 41725  
QY 858 TAATAATGATAATAACAAAACCTGTTGTTTCTTTCCTTCA 896  
Db 41726 TAATAATGATAATAACAAAACCTGTTGTTTCTTTCCTTCA 41764

RESULT 13  
MDO251117  
LOCUS MDO251117 1065 bp mRNA linear PLN 16-NOV-2001  
DEFINITION Malus domestica mRNA for C-type MADS box protein (mads14 gene).  
ACCESSION AJ251117  
VERSION AJ251117.1 GI:16973295  
KEYWORDS C-type MADS box protein; mads14 gene.  
SOURCE apple tree.  
ORGANISM Malus x domestica  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

REFERENCE 1  
AUTHORS Vosman,B. and Smulders,M.J.M.  
TITLE Isolation of apple B- and C-type MADS box genes from vegetative tissue  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1065)  
AUTHORS van der Linden,C.G.  
TITLE Direct Submission  
JOURNAL Submitted (15-NOV-1999) van der Linden C.G., Identity and Genetic Diversity, CPRO Wageningen University & Research Centre, PO Box 16, Wageningen, 6700 AA, NETHERLANDS  
FEATURES  
source Location/Qualifiers  
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140..868  
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BASE COUNT 344 a 237 c 211 g 273 t  
ORIGIN  
Query Match 37.2%; Score 333.6; DB 8; Length 1065;  
Best Local Similarity 69.4%; Pred. No. 6.2e-81;  
Matches 491; Conservative 0; Mismatches 199; Indels 18; Gaps 2;  
QY 46 AAGAAACTAGGAGAGGGGAAAATACAGATAAAGAGGATAGAGACACACAATCGTCAA 105  
Db 179 AAAAAATTGGGAAGAGGCAAAATTGAGATTAAAGCGGATCGAAAACACTACCAATCGACAA 238  
QY 106 GTTACTTTCGCAACAGCGCAATGGTCTTCTCAAGAAAGCTTATGAACCTCTCTGTCTTG 165  
Db 239 GTCACCTTTCGCAACAGCGCGCAACCGATTCTTAAGAAAGCCTATGAATTGCTGTTCT 298  
QY 166 TGTGATGCCGAAGTTGCCCTCGTCATCTTCTCCACTCGTGGCCCTCTCTATGATAGCGCC 225  
Db 299 TGTGATGCTGAAGTTGCTCTTATCGTCTTCTCCACCGTGGCCGCTCTATGATGATGCT 358  
QY 226 AACACAGTGTGAGGGGTACAATTTGAAAGGTACAGAAAGCTTGTTCGGATGCCGTCAAC 285  
Db 359 AACACAGCGTTAGAGCAACAATCGACAGGTACAAAAAGCATGCGCTGATTCTACGGAC 418  
QY 286 CCTCCTTCCGTCACCGAAGCTAATACTAGTACTATCAGCAAGAGCCTCTAAGCTTCGG 345  
Db 419 GGTGGATCTGTATCAGAAGCTAACACTCAGTCTTTATCAGCAGGAAGCATCAAAACTGCCA 478  
QY 346 AGGCAGATTCGAGATATTCAGAAATCAAATPAGGCATATTTGTTGGGAATCAGCTTGGTTC 405  
Db 479 AGACAGATCCGAGAAATTCAGAAATTCAAACAGGCATATATCTGGGGAAATCCCTTAGCACC 538  
QY 406 TTGAAGTTCAGAGGAAGCTCAAAAAACCTAGAAAGCGCTCTTGAAGAAAGGAATCAGCGGTGC 465  
Db 539 TTGAAGTTCAGAGGAAGCTCAAAAAACCTAGAAAGGAATTTGGAGAAAGGAATCAGCAGAATA 598  
QY 466 CGCTCCAAAAGAATCAGCTGTTAGTGGCAGATAGAGTATATCGAAGAGAGGGAATG 525  
Db 599 AGATCCAAAAGAATGAAATCCTGTTTCTGAAATCGAATTTCATGCAAAAGAGGAGAGACT 658  
QY 526 GAGTTGCAACACAATTAACATGTAACCTGCGGACCAAGATAGCCGAGGCGGCAGATTGAAT 585  
Db 659 GAGCTGCAACACCACACAATTTTCTGAGAGCAAAAGATAGCTGAAAGCGGAGAG---GGAA 715

Rosidae; eurosids I; Rosales; Rosaceae; Maloideae; Malus.





GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 2, 2003, 08:21:19 ; Search time 1738.09 Seconds  
(without alignments)  
8935.939 Million cell updates/sec

Title: US-09-978-382A-5  
Perfect score: 959  
Sequence: 1 gaattcatcttccatctc.....ccaagagacggttacacaaa 959

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST.\*

1: em\_estba.\*

2: em\_esthum.\*

3: em\_estin.\*

4: em\_estnu.\*

5: em\_estov.\*

6: em\_estpl.\*

7: em\_estro.\*

8: em\_htc.\*

9: gb\_est1.\*

10: gb\_est2.\*

11: gb\_htc.\*

12: gb\_est3.\*

13: gb\_est4.\*

14: gb\_est5.\*

15: em\_estfun.\*

16: em\_estom.\*

17: gb\_gss.\*

18: em\_gss\_hum.\*

19: em\_gss\_inv.\*

20: em\_gss\_pln.\*

21: em\_gss\_vrt.\*

22: em\_gss\_fun.\*

23: em\_gss\_mam.\*

24: em\_gss\_mus.\*

25: em\_gss\_other.\*

26: em\_gss\_pro.\*

27: em\_gss\_rod.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID          | Description        |
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| c 1        | 451   | 47.0        | 615    | 10 AV557878 | AV557878 AV557878  |
| c 2        | 397   | 41.4        | 452    | 9 AU227814  | AU227814 AU227814  |
| c 3        | 385   | 40.1        | 537    | 10 AV556852 | AV556852 AV556852  |
| 4          | 331.4 | 34.6        | 686    | 14 BQ411600 | BQ411600 GA_EG004  |
| 5          | 329.8 | 34.4        | 656    | 14 BQ411583 | BQ411583 GA_EG004  |
| 6          | 328.4 | 34.2        | 748    | 13 BI311095 | BI311095 EST531284 |

|    |       |      |     |             |                    |
|----|-------|------|-----|-------------|--------------------|
| 7  | 318.4 | 33.2 | 754 | 13 BI310910 | BI310910 EST531266 |
| 8  | 316.2 | 33.0 | 636 | 14 BQ123247 | BQ123247 EST608823 |
| 9  | 308   | 32.1 | 624 | 10 AW277843 | AW277843 sf67d01.y |
| 10 | 304.6 | 31.8 | 555 | 13 BI272847 | BI272847 NF097G09F |
| 11 | 301.6 | 31.4 | 548 | 10 AW277299 | AW277299 sf80e05.y |
| 12 | 298.8 | 31.2 | 656 | 10 BE659918 | BE659918 1299 Gmax |
| 13 | 292.4 | 30.5 | 776 | 12 BG445079 | BG445079 GA_Ea002  |
| 14 | 292.4 | 30.5 | 866 | 12 BG441292 | BG441292 GA_Ea001  |
| 15 | 292.4 | 30.5 | 892 | 12 BG444639 | BG444639 GA_Ea002  |
| 16 | 292.2 | 30.5 | 715 | 13 BI933168 | BI933168 EST553057 |
| 17 | 290   | 30.2 | 848 | 12 BG445047 | BG445047 GA_Ea002  |
| 18 | 288.6 | 30.1 | 642 | 9 AI725968  | AI725968 BNLGH1137 |
| 19 | 285.6 | 29.8 | 597 | 9 AI729115  | AI729115 BNLGH1126 |
| 20 | 285   | 29.7 | 632 | 10 AW185524 | AW185524 se80h09.y |
| 21 | 279.8 | 29.2 | 754 | 9 AI731375  | AI731375 BNLGH1938 |
| 22 | 279.8 | 29.2 | 761 | 9 AI731368  | AI731368 BNLGH1937 |
| 23 | 279.6 | 29.2 | 649 | 10 AW184799 | AW184799 se82f12.y |
| 24 | 278.8 | 29.1 | 548 | 10 BE434089 | BE434089 EST405167 |
| 25 | 278   | 29.0 | 607 | 10 AW705451 | AW705451 SK49c05.y |
| 26 | 276.2 | 28.8 | 538 | 10 BE433121 | BE433121 EST399650 |
| 27 | 274.4 | 28.6 | 562 | 9 AI727662  | AI727662 BNLGH1854 |
| 28 | 274   | 28.6 | 698 | 10 BE659915 | BE659915 7-H4 Gmax |
| 29 | 271.8 | 28.3 | 597 | 10 AW704750 | AW704750 SK55a06.y |
| 30 | 271.4 | 28.3 | 608 | 10 AW278878 | AW278878 sf99h09.y |
| 31 | 269   | 28.1 | 566 | 9 AI728519  | AI728519 BNLGH1109 |
| 32 | 267   | 27.8 | 754 | 13 BI311053 | BI311053 EST531280 |
| 33 | 266.4 | 27.8 | 960 | 12 BG445265 | BG445265 GA_Ea002  |
| 34 | 261.4 | 27.3 | 802 | 13 BI925669 | BI925669 EST545558 |
| 35 | 260.2 | 27.1 | 539 | 9 AI771796  | AI771796 EST252896 |
| 36 | 259.4 | 27.0 | 584 | 12 BG442607 | BG442607 GA_Ea001  |
| 37 | 259.2 | 27.0 | 885 | 14 BQ796770 | BQ796770 EST 5708  |
| 38 | 257.4 | 26.8 | 600 | 9 AI728967  | AI728967 BNLGH1121 |
| 39 | 256.2 | 26.7 | 586 | 12 BG446848 | BG446848 GA_ED003  |
| 40 | 255.6 | 26.7 | 537 | 9 AI486290  | AI486290 EST244611 |
| 41 | 255   | 26.6 | 558 | 10 AW705789 | AW705789 sk51h05.y |
| 42 | 255   | 26.6 | 613 | 10 BE659913 | BE659913 3-D9 Gmax |
| 43 | 254.8 | 26.6 | 929 | 12 BG444491 | BG444491 GA_Ea002  |
| 44 | 251.4 | 26.2 | 498 | 12 BF112843 | BF112843 EST440433 |
| 45 | 249   | 26.0 | 892 | 12 BG415259 | BG415259 HVSMEK000 |

#### ALIGNMENTS

RESULT 1  
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LOCUS AV557878 615 bp mRNA linear EST 07-SEP-2000  
DEFINITION Arabidopsis thaliana green siliques Columbia Arabidopsis thaliana cDNA clone SQ083b07F 3', mRNA sequence.  
ACCESSION AV557878  
VERSION AV557878.1 GI:8729293  
KEYWORDS EST.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE 1 (bases 1 to 615)  
AUTHORS Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.  
TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries  
JOURNAL DNA Res. 7, 175-180 (2000)  
MEDLINE 20363093  
COMMENT Contact: Erika Asamizu  
The First Laboratory for Plant Gene Research  
Kazusa DNA Research Institute  
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan  
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.  
FEATURES  
Location/Qualifiers  
1..615  
/organism="Arabidopsis thaliana"  
/strain="Columbia"





The First Laboratory for Plant Gene Research  
Kazusa DNA Research Institute  
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan  
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

## FEATURES

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/organism="Arabidopsis thaliana"  
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XhoI"

BASE COUNT 144 a 106 c 102 g 185 t

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Query Match 40.1%; Score 385; DB 10; Length 537;  
Best Local Similarity 100.0%; Pred. No. 3.2e-103;  
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 477 TTGAACCTTAAGGAACCTCAAGAACCTTGAAAGTAGGCTTGAGAAAGGAATCAGTCGTGTC 536  
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QY 717 CACCAAGTCCGAGCAGTATAACCGGAATTATATGCGGTAACTTCTTGAACCGAATCAG 776  
Db 297 CACCAAGTCCGAGCAGTATAACCGGAATTATATGCGGTAACTTCTTGAACCGAATCAG 238  
QY 777 AATTCCTCCAAACCAAGACCAACCACTCTGCAACTTGTGATTCAGTCTACATAGCT 836  
Db 237 AATTCCTCCAAACCAAGACCAACCACTCTGCAACTTGTGATTCAGTCTACATAGCT 178  
QY 837 TCTTTCTCAGCTGAGATCGATCT 861  
Db 177 TCTTTCTCAGCTGAGATCGATCT 153

## RESULT 4

BQ411600 686 bp mRNA linear EST 22-MAY-2002  
LOCUS GA\_Ed0041B08f Gossypium arboreum 7-10 dpa fiber library Gossypium  
DEFINITION arboreum cdna clone GA\_Ed0041B08f, mRNA sequence.  
BQ411600  
ACCESSION BQ411600.1 GI:21099287  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Gossypium arboreum.  
Gossypium arboreum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.  
1 (bases 1 to 686)

Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry  
D., Wood, F.C., Leslie, A. and Wilkins, T.A.  
An integrated analysis of the genetics, development, and evolution  
of the cotton fiber  
Unpublished (2000)

## JOURNAL

COMMENT  
Contact: Wing RA  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA

## RESULT 5

BQ411583  
LOCUS  
DEFINITION  
ACCESSION

BQ411583 656 bp mRNA linear EST 22-MAY-2002  
GA\_Ed0041A08f Gossypium arboreum 7-10 dpa fiber library Gossypium  
arboreum cdna clone GA\_Ed0041A08f, mRNA sequence.  
BQ411583

Tel: 864 656 7288  
Fax: 864 656 4293  
Email: rwing@clemsun.edu  
Total High Quality bases = 612  
Seq primer: TAATACGACTCACTATAGG  
High quality sequence start: 2  
High quality sequence stop: 685.  
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Location/Qualifiers  
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Matches 425; Conservative 0; Mismatches 156; Indels 0; Gaps 0;  
QY 117 AAGAAGATAGGAGAGGGAAGATAGAGATAAGAGATAGAGAACTACGAATCGTCAA 176  
Db 57 AAAAAATGGGAAGGCAAAATCGAGATTAAAGCGATCGAGAACACCCTAATCGACAA 116  
QY 177 GTCACCTTCTGCAACGACGCAATGTTTACTCAAGAAAGCTTATGAGCTCTCTGTTG 236  
Db 117 GTTACCTTCTGCAAGCGCGCAATGAGCTGTCAAAAGGCTATGAATTATCTGTTCT 176  
QY 237 TGTGACGCTGAGGTTGCTTGTCTCTCTCCACTCGAGGCCGCTCTACGAGTAGCGC 296  
Db 177 TGTGATGCTGAGGTTGCTCTCATAGTCTTCCAGCGCTGCTCTATGAATATGCT 236  
QY 297 AACACAGTGTGAGAGGAACAATAGAAAGTACAGAAAGCTTGCTCCGAGCCGCTTAAC 356  
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Db 417 TTGACCTTAAAGGAACCTCAAGAACCTTGAGGCGGCTTGAGAAAGGCAATTTGTAATC 476  
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Db 83 AAGAAATGGGAAGAGGAAAAATGAAATCAAGAGGATTGAAACACATACCAATAGGCAA 142
QY 177 GTCACTTTCTGCAAAACGAGCAATGGTTTACTCAAGAAGCTTATGAGCTCTCTGCTGTG 236
Db 143 GTCACTTTTTCAAACGAGCAATGGATTGTTGAAGAAGCTTATGAATATATCCGTTCTT 202
QY 237 TGTGACGCTGAGTTGCTTCTTGTCACTTCTCTCACTCGAGCGCTCTCTACGAGTACGCC 296
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QY 297 AACAAAGTGTGAGAGGAACAATAGAAAGGTACAAGAGCTTCTCCGACGCGGTTAAAC 356
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BI310910
LOCUS
DEFINITION EST5312660 GESD Medicago truncatula cDNA clone pgESD9K22 5' end,
mRNA sequence.
ACCESSION BI310910
VERSION BI310910.1 GI:14985237
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1 (bases 1 to 754)
Grusak,M.A., Samac,D.A., Town,C.D., Van Aken,S., Utterback,T., Cho
,J. and Fraser,C.M.
ESTs from developing reproductive tissues of Medicago truncatula
Unpublished (2001)
Contact: Michael A. Grusak
USDA/ARS Children's Nutrition Research Center
Baylor College of Medicine
1100 Bates Street, Houston, TX 77030-2600, USA
Tel: 713-798-7044
Fax: 713-798-7078
Email: mgrusak@bcm.tmc.edu
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B397765e

TIGR sequence name: MTPAN717K  
More information is available at: www.medicago.org  
Seq primer: SKmod (CTA gaa cta gta gat CC).

## FEATURES

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pollination"

/note="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2:  
XhoI; Immature seeds, collected from pods ranging in age  
from 11 to 19 days after pollination, were harvested from  
greenhouse-grown plants. Seeds were removed and  
separated from pod walls and were immediately frozen in  
liquid nitrogen. Seeds throughout the age range were  
pooled for mRNA extraction. cDNA was prepared from polyA+  
enriched RNA. The cDNA was directionally ligated into  
the Unizap XR vector from Stratagene and packaged using  
Gigapack III Gold packaging extracts. Plasmids containing  
cDNA inserts were excised from the recombinant lambda-Zap  
phage using Ex-assist helper phage and propagated in  
XL0LR cells."

BASE COUNT 245 a 144 c 159 g 206 t  
ORIGIN

Query Match 33.2%; Score 318.4; DB 13; Length 754;  
Best Local Similarity 68.9%; Pred. No. 2.1e-83;  
Matches 471; Conservative 0; Mismatches 201; Indels 12; Gaps 2;

QY 139 TAGAGATAAGAGGATAGAGAACTACTACGAATCGTCAAGTCACTTTCTGCAAAACGACGCA 198  
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QY 319 TAGAAAGGTACAAGAAAGCTTGTCTCCGACCGCTTAACCTCCGACCATCACCCGAAGCTA 378  
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QY 379 ATACTCAGTACTATCAGCAAGAGCGCTCAAACTCCGGAGACAGATTCCGGGACATTTCAGA 438  
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QY 439 ATTTGAACAGACACATCTTGTGTTGAATCTCTTGGTTCCCTTGAACITTAAGGAACCTCAAGA 498  
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QY 499 ACCTTGAAGTAGGCTTGAGAAAGGAATCAGTCTGTCGATCCGATCCAAAGACACGAGATGT 558  
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QY 559 TAGTTGCAGAGATTGAATACATGCAAAAAGGAAATCGAGCTGCAAAAACGATTAACATGT 618  
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QY 619 ATCTCCGCTCCAGATTTACTGAAAGAACAGGTCTACAGCAACAACAAGATCCAGTGTGATAC 678  
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QY 679 ATCAAGGGACAGTTTACGAGTCGGGTGTTACTTCTTCTCACCAGTCGGGGCAGTATAACC 738  
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165 TGTCATCGCGAAGTGCCTTGTCTCTCTCACCTCGCGTGGTTGTATGATGATGCC 224
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357 CCTCCGACCATCACCGAAGCTAATCTAGTACTAGTACAGCAAGAGCGCTCTAACTCCGG 416
285 GCAGAACTCTGTATCTGAGCTAATACCCAGTCTTACCAGCAAGAAATCATCCAATTGAGA 344
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525 GAGCTGCAAAACCAATAACAATTATCTACG 553

RESULT 11
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DEFINITION Gm-c1019-2457 5' similar to SW:AGL5_ARATH P29385 FLORAL HOMEOTIC
PROTEIN AGL5. ;, mRNA sequence.
ACCESSION AW277299.1 GI:6665849
VERSION AW277299
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE 1 (bases 1 to 548)
AUTHORS Shoemaker,R., Kelm,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 949 Std Error: 0.00
Seq primer: -40RP from Gibco
High quality sequence stop: 438.
FEATURES
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/tissue_type="immature seed coats of greenhouse grown
plants"

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/lab_host="DH10B (Gibco BRL)"
/Note="Vector: pSPORT1 (Life Technologies); Site_1: Not I;
Site_2: Sal I; This cdna library was constructed from mRNA
isolated from immature seed coats (200-300 mgs) of
greenhouse grown plants. The library was prepared using
the Life technologies pSuperScript cdna library
construction kit. Complementary DNA was synthesized from
mRNA using a poly (dT) sequence with a Not I restriction
site. Sal I linker adapters were ligated to the
blunt-ended cdna fragments followed by Not I digestion.
The cdna fragments were directionally cloned into the Not
I-Sal I restriction site of the pSPORT1 vector. The
ligated cdna fragments were transformed into E.coli
ElectroMax DH10B host cells (Gibco BRL). This library was
constructed by Dr. Lila Vodkin and Dr. Anu Khanna."

BASE COUNT 187 a 107 c 128 g 126 t
ORIGIN

Query Match 31.4%; Score 301.6; DB 10; Length 548;
Best Local Similarity 71.9%; Pred. No. 1.9e-78;
Matches 394; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

QY 127 GGAGAGGGAAGATAGAGATAAAGAGGATAGAGACACTACGATCGTCAAGTCACCTTCT 186
Db 1 GAAGAGGGAAGATTGAATCAAAACGGATCGAGAACACCAACCAATAGGCAAGTCACCTTCT 60
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QY 667 CGAGTGTG 674
Db 541 CAAATATG 548

RESULT 12
BE659918
LOCUS BE659918 656 bp mRNA linear EST 06-SEP-2000
DEFINITION 1299 GmaxSC Glycine max cdna, mRNA sequence.
ACCESSION BE659918
VERSION BE659918.1 GI:9985912
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```



Spermatophyta; Magnoliophyta; eudicotyledons; core eucots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

|           |                                                  |
|-----------|--------------------------------------------------|
| REFERENCE | 1 (bases 1 to 656)                               |
| AUTHORS   | Harris,N., Chapman,B.P. and Gijzen,M.            |
| TITLE     | Gene expression in developing soybean seed coats |
| JOURNAL   | Unpublished (2000)                               |
| COMMENT   | Contact: Gijzen M                                |

## FEATURES

source

| location/qualifiers                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | source                     |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------|
| 1. .656                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |                            |
| /organism="Glycine max"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |                            |
| /cultivar="Harosoy 63"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                            |
| /db_xref="taxon:3847"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                            |
| /clone_lib="GmaxSC"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                            |
| /tissue_type="Seed coats"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                            |
| /lab_host="E. coli strain XL0LR"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |                            |
| /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed from polyA+ enriched mRNA from green seed coats in mid to late developmental stage , average fresh weight 250 mg per seed. Traces of pod and embryo tissue also present. Complementary DNA was synthesized from mRNA using an XhoI-poly(dT) linker-primer. EcoRI adapters were ligated to the blunt-ended cDNA fragments and the products were digested with XhoI for directional cloning into lambda ZAP Express vector. This lambda library was amplified once using E. coli host strain XL1 Blue MRF'. Inserts were then subcloned by mass excision using ExAssist helper phage for conversion into phagemid vector pBK-CMV in E. coli host strain XL0LR." |                            |
| 225 a                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 129 c 148 g 152 t 2 others |
| BASE COUNT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |                            |

|            |       |       |       |       |          |
|------------|-------|-------|-------|-------|----------|
| BASE COUNT | 225 a | 129 c | 148 g | 152 t | 2 others |
| ORIGIN     |       |       |       |       |          |

Query Match 31.2%; Score 298.8; DB 10; Length 656;  
Best Local Similarity 69.5%; Pred. No. 1.4e-77;

68 GCTTATAGAAATGGAGGGTGGTCCGAGTAATGAAGTAGCAGAGAGCAGCAAGAAGATAGG 127

db  
40 GCTTGCAACCATGGGCGATCCAAATCAGCTTCACACCCCTTCTGCCTGC

128 GAGAGGGAAGATAGAGATAAAGAGGATAGAGAACACTACGAATCGTCAAGTCACITTCG 187

db

QY 188 CAAACGACGCAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGTCTTGTGTGACGCTGA 247

[illegible]

248 GGTGGCTCTTGTCACTCTTCTCCACTCGAGGCCGCTCTCTACGAGTACGCCAACACAGTGT 307

db 220 AGTTGCCCTTGTTGTCTCTCAACCCGTGGCCGTTTGATGAGTATCCCAACAACACTCT

308 GAGAGGAACAATAGAAAGGTACAAGAAAGCTTGCTCCGACGCCGTTAACCCCTCCGACCAT 367

Db 280 TAGGGCCACTATTGAGAGGTACAAGAAGGCAAAATGCTGCTGCTTCAACGCAGAAATCCCT 330

368 CACCGAAGCTAATACTCAGTACTATCAGCAAGAGGGGTCCTAAACTCCGGAGACAGATTTCG 427

db 340 ATCTGAAGCTAACACACACAGTTTTACCGCAAGAGTCATCCAAATTTGAGAAGACATATATCC 389

428 GGACATTCAGAATTTGAACAGACACATTCCTTGGTGAATCTCTTGGTTCCTTGAACCTTAA 487

b  
400 AGATATTTCAGAACTTAAACAGGCCACATCCCTTTGGTGAGGCACTTTGGTTCTCCTCGAGCTCTCAA

488 GGAAGCTCAAGAACCTTTGAAAGTAGGCTTGAGAAAGGAATCAGTCGTTCGATCCAGAA 547

db 460 GGACTAAAGAACCTCGAGGGTAGATTGGAGAAAGGATTAAGCAGAGTTTGTAGTCTAGAAA 519



|             |                                                                         |                                                                |                    |
|-------------|-------------------------------------------------------------------------|----------------------------------------------------------------|--------------------|
| QY          | 297                                                                     | AACAACAGTGTGAGAGGAACAATAAGAGGTACAAGAGCTTGCTCCGACGCCGTTAAAC     | 356                |
| Db          | 285                                                                     |                                                                |                    |
| QY          | 357                                                                     | CCTCCGACCATCACCGAAGCTAATACTCAGTACTATCAGCAAGAGCGCTCTAAACTCCGG   | 416                |
| Db          | 345                                                                     | ACAAACACTGTGTACTGAAATCAATGCTCAGTATTATCAACAAGAAATCAGCCAAGTTGAGA | 404                |
| QY          | 417                                                                     | AGACAGATTCGGGACATTCAGAATTGACAGACACATCTTGGTGAATCTCTTGGTTCC      | 476                |
| Db          | 405                                                                     |                                                                |                    |
| QY          | 477                                                                     | TGAACTTTAAGGAACTCAAGAACCTTGAAGTAGGCTTGAGAAAGGAATCAGTCGTC       | 536                |
| Db          | 465                                                                     | TTAACTGTGAAGAGTTAAGCAGGTAGAAACAGGCTTGAAGAGGAATTACTAGGATC       | 524                |
| QY          | 537                                                                     | CGATCCAAGAACGACGAGATGTTAGTTGCAGAGATTGAATACATGCAAAAAAGGAAATC    | 596                |
| Db          | 525                                                                     | AGGTCCAAAGACGAGAAATGCTACTAGCTGAAATAGAGTTTTTGCAGAAAGGGAATC      | 584                |
| QY          | 597                                                                     | GAGCTGCAAAACGATAACATGTATCTCCGCTCCAGAGATTACTGAAAGAACAGGTCACAG   | 656                |
| Db          | 585                                                                     | GAATTGGAAAATGAAAGTGTGTGCTCCGAACCAAGATTGCAGAAATTGAGAGGCTTCAG    | 644                |
| QY          | 657                                                                     | CA 658                                                         |                    |
| Db          | 645                                                                     | CA 646                                                         |                    |
| RESULT 14   |                                                                         |                                                                |                    |
| LOCUS       | BG441292                                                                |                                                                |                    |
| DEFINITION  | GA_Ea0012J14f Gossypium arboreum 7-10 dpa fiber library Gossypium       | linear                                                         | EST 15-MAR-2001    |
| ACCESSION   | BG441292                                                                |                                                                |                    |
| VERSION     | BG441292.1                                                              | GI:13350932                                                    |                    |
| KEYWORDS    | EST.                                                                    |                                                                |                    |
| SOURCE      | Gossypium arboreum.                                                     |                                                                |                    |
| ORGANISM    | Gossypium arboreum                                                      |                                                                |                    |
| REFERENCE   | 1 (bases 1 to 866)                                                      |                                                                |                    |
| AUTHORS     | Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry |                                                                |                    |
| TITLE       | D., Wood, T.C., Leslie, A. and Wilkins, T.A.                            |                                                                |                    |
| JOURNAL     | An integrated analysis of the genetics, development, and evolution      |                                                                |                    |
| COMMENT     | of the cotton fiber                                                     |                                                                |                    |
| FEATURES    | Unpublished (2000)                                                      |                                                                |                    |
| source      | Contact: Wing RA                                                        |                                                                |                    |
|             | Clemson University Genomics Institute                                   |                                                                |                    |
|             | Clemson University                                                      |                                                                |                    |
|             | 100 Jordan Hall, Clemson, SC 29634, USA                                 |                                                                |                    |
|             | Tel: 864 656 7288                                                       |                                                                |                    |
|             | Fax: 864 656 4293                                                       |                                                                |                    |
|             | Email: rwing@clemson.edu                                                |                                                                |                    |
|             | Seq primer: TAATACGACTCATATAGGG                                         |                                                                |                    |
|             | High quality sequence stop: 676.                                        |                                                                |                    |
|             | Location/Qualifiers                                                     |                                                                |                    |
|             | 1..866                                                                  |                                                                |                    |
|             | /organism="Gossypium arboreum"                                          |                                                                |                    |
|             | /strain="AKA"                                                           |                                                                |                    |
|             | /cultivar="8400"                                                        |                                                                |                    |
|             | /db_xref="taxon:29729"                                                  |                                                                |                    |
|             | /clone="GA_Ea0012J14f"                                                  |                                                                |                    |
|             | /clone_lib="Gossypium arboreum 7-10 dpa fiber library"                  |                                                                |                    |
|             | /tissue_type="Fibers isolated from bolls harvested 7-10                 |                                                                |                    |
|             | dpa"                                                                    |                                                                |                    |
|             | /lab_host="E. coli"                                                     |                                                                |                    |
|             | /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"                    |                                                                |                    |
| BASE COUNT  | 297 a 158 c 188 g 218 t                                                 | 5 others                                                       |                    |
| ORIGIN      |                                                                         |                                                                |                    |
| Query Match | 30.5%                                                                   | Score 292.4;                                                   | DB 12; Length 866; |

|                       |                                                                         |                                                                 |                                      |
|-----------------------|-------------------------------------------------------------------------|-----------------------------------------------------------------|--------------------------------------|
| Best Local Similarity | 71.2%                                                                   | Pred. No. 1.2e-75;                                              |                                      |
| Matches               | 386;                                                                    | Conservative                                                    | 0; Mismatches 156; Indels 0; Gaps 0; |
| QY                    | 117                                                                     | AAGAAGATAGGAGAGGAAGATAGAGATAAGAGGATAGAGAACACTACGAAATCGTCAA      | 176                                  |
| Db                    | 38                                                                      | AAGAAGATGGGAAGAGGAAAAATAGAGATAAGAGGATCGAAAAACAACAATCGTCAG       | 97                                   |
| QY                    | 177                                                                     | GTCACCTTTCTGCAAAAGCAGCGCAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGCTTG  | 236                                  |
| Db                    | 98                                                                      | GTTACCTTTTGCAAAACGAGGAATGGCCTGCTGAAGAAAGCTTACGAACTGTCACTCTG     | 157                                  |
| QY                    | 237                                                                     | TGTGACGCTGAGGTGCTTGTCTCTCTCATCTCTCCACTCGAGGCGCTCTACAGTACGCC     | 296                                  |
| Db                    | 158                                                                     | TGTGATGCTGAAAGTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT     | 217                                  |
| QY                    | 297                                                                     | AACAACAGTGTGAGAGGAACAATAAGAGGTACAAGAAAGCTTGTCTCGACGCCGTTAAAC    | 356                                  |
| Db                    | 218                                                                     | AACAACAACATAAGATCAACAATAGACAGGTACAAGAGGCTTGTCTCAGATCTTCTAAAC    | 277                                  |
| QY                    | 357                                                                     | CCTCCGACCATCACCGAAGCTTAATCTCAGTACTATCAGCAAGAGGCGTCTTAACTCCGG    | 416                                  |
| Db                    | 278                                                                     | ACAAACACTGTTTACTGAAATCAATGCTCAGTATTATCAACAAGAAATCAGCCAAAGTTGAGA | 337                                  |
| QY                    | 417                                                                     | AGCAGATTTCGGGACATTCAGAATTGAAACAGACACATCTTGGTGAATCTCTTGGTTCC     | 476                                  |
| Db                    | 338                                                                     | CAGCAGATTCAAAATGTTACAGAAATCTAACAGGCACTTAATGGAGATCTCTTGAGTTCC    | 397                                  |
| QY                    | 477                                                                     | TTGAACCTTTAAGGAACTCAAGAACCTTGAAGTAGGCTTGAGAAAGGAATCAGTCGTC      | 536                                  |
| Db                    | 398                                                                     | TTAACTGTGAAGAGAGTTAAAGCAGGTAGAAAACAGGCTTGAAGAGGAATCTAGGATC      | 457                                  |
| QY                    | 537                                                                     | CGATCCAAGAACGACGAGATGTTAGTTGCAGAGATTGAATACATGCAAAAAAGGAAATC     | 596                                  |
| Db                    | 458                                                                     | AGGTCCAAAGACGCAAAATGCTACTAGCTGAATAGAGTTTTTGCAGAAAGGGAATC        | 517                                  |
| QY                    | 597                                                                     | GAGCTGCAAAACGATAACATGTATCTCCGCTCCAGAGTACTGAAAGAACAGGTCACAG      | 656                                  |
| Db                    | 518                                                                     | GAATTGGAAAATGAAAGTGTGTGCTCCGAACCAAGATTGCAGAAATTGAGAGGCTTCAG     | 577                                  |
| QY                    | 657                                                                     | CA 658                                                          |                                      |
| Db                    | 578                                                                     | CA 579                                                          |                                      |
| RESULT 15             |                                                                         |                                                                 |                                      |
| LOCUS                 | BG444639                                                                |                                                                 |                                      |
| DEFINITION            | GA_Ea0025A08f Gossypium arboreum 7-10 dpa fiber library Gossypium       | linear                                                          | EST 15-MAR-2001                      |
| ACCESSION             | BG444639                                                                |                                                                 |                                      |
| VERSION               | BG444639.1                                                              | GI:13354291                                                     |                                      |
| KEYWORDS              | EST.                                                                    |                                                                 |                                      |
| SOURCE                | Gossypium arboreum.                                                     |                                                                 |                                      |
| ORGANISM              | Gossypium arboreum                                                      |                                                                 |                                      |
| REFERENCE             | 1 (bases 1 to 892)                                                      |                                                                 |                                      |
| AUTHORS               | Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry |                                                                 |                                      |
| TITLE                 | D., Wood, T.C., Leslie, A. and Wilkins, T.A.                            |                                                                 |                                      |
| JOURNAL               | An integrated analysis of the genetics, development, and evolution      |                                                                 |                                      |
| COMMENT               | of the cotton fiber                                                     |                                                                 |                                      |
|                       | Unpublished (2000)                                                      |                                                                 |                                      |
|                       | Contact: Wing RA                                                        |                                                                 |                                      |
|                       | Clemson University Genomics Institute                                   |                                                                 |                                      |
|                       | Clemson University                                                      |                                                                 |                                      |
|                       | 100 Jordan Hall, Clemson, SC 29634, USA                                 |                                                                 |                                      |
|                       | Tel: 864 656 7288                                                       |                                                                 |                                      |
|                       | Fax: 864 656 4293                                                       |                                                                 |                                      |
|                       | Email: rwing@clemson.edu                                                |                                                                 |                                      |
|                       | Seq primer: TAATACGACTCATATAGGG                                         |                                                                 |                                      |
|                       | High quality sequence stop: 685.                                        |                                                                 |                                      |

| FEATURES              | source | Location/Qualifiers                                                 |
|-----------------------|--------|---------------------------------------------------------------------|
|                       |        | 1. .892                                                             |
|                       |        | /organism="Gossypium arboreum"                                      |
|                       |        | /strain="AKA"                                                       |
|                       |        | /cultivar="8400"                                                    |
|                       |        | /db_xref="taxon:29729"                                              |
|                       |        | /clone="GA_Ea0025A08f"                                              |
|                       |        | /clone_lib="Gossypium arboreum 7-10 dpa fiber library"              |
|                       |        | /tissue_type="Fibers isolated from bolls harvested 7-10 dpa"        |
|                       |        | /lab_host="E. coli"                                                 |
|                       |        | /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"                |
| BASE COUNT            | 303 a  | 161 c 192 g 223 t 13 others                                         |
| ORIGIN                |        |                                                                     |
| Query Match           | 30.5%; | Score 292.4; DB 12; Length 892;                                     |
| Best Local Similarity | 71.2%; | Pred. No. 1.2e-75;                                                  |
| Mismatches            | 386;   | Conservative 0; Mismatches 156; Indels 0; Gaps 0;                   |
| QY                    | 117    | AAGAAGATAGGAGAGGGAACATAGAGATAAAGAGGATAGAGAACACTACGAATCGTCAA 176     |
| DB                    | 89     | AAGAGAAATGGGAAGAGGAAAAATAGAGATAAAGAGGATCGAAAAACACAAATCGTCAG 148     |
| QY                    | 177    | GTCACCTTCTCCAAACGACGCAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGCTTG 236     |
| DB                    | 149    | GTTACCTTTTGCAACACGAGGAATGGCGTGCTGAAGAAAGCTTACGAACCTGTCTGCTG 208     |
| QY                    | 237    | TGTGACGCTAGGTTGCTTGTCTCATCTTCTCCACCTCGAGGCCGTCTCTACGAGTACGCC 296    |
| DB                    | 209    | TGTGATGCTGAAGTTGCTCTCATTTGCTTCTCCAGTCGAGGCCGTCTGTATGAGTACTCC 268    |
| QY                    | 297    | AACAACAGTGTGAGAGGAACAATAGAAAAGGTACAAGAAAGCTTGCTCCGACGCCGTTAAAC 356  |
| DB                    | 269    | AACAACAATTAAGATCAACAATAGACAGGTACAAGAGGCTTGCTCAGATACTTCTTAAC 328     |
| QY                    | 357    | CCTCCGACCATCACCGAAGCTTAATACTCAGTACTATCAGCAAGAGCGCTCTAAACTCCGG 416   |
| DB                    | 329    | ACAACACACTGTTACTGAAATCAATGCTCAGTATTATCAACAAGAATCAGCCAAGTTGAGA 388   |
| QY                    | 417    | AGACAGATTCCGGACATTCAGNAATTTCAACAGACACACATTCYTGGTGAATCTCTTGGTTCC 476 |
| DB                    | 389    | CAGCAGATTCAAAATGTTACAGAATTTCAACAGGCACCTAATGGGAGATTCCTTGAGTTCC 448   |
| QY                    | 477    | TTGAACCTTAGGAACCTCAAGAACCTTGAAGTAGGCTTGAGAAAGGAATCAGTCGTGTC 536     |
| DB                    | 449    | TTAACTGTGAAAGAGTTAAAGCAGGTAGAAAACAGGGCTTGAAGAGGGAATTAAGTAGGATC 508  |
| QY                    | 537    | CGATCCAAGAAGCACGAGATGTTAGTTGCAGAGATTGAATACATGCAAAAAAGGGAAATC 596    |
| DB                    | 509    | AGGTCCAAGAAGCACGNAATGCTACTAGCTGAATAGAGTTTTCGACAGAAAGGGAAATC 568     |
| QY                    | 597    | GAGTCGAAAACGATTAACATGTATCTCCGCTCCAAGATTACTCAAGAACACAGCTCTACAG 656   |
| DB                    | 569    | GAATTGGAAAAATGAAGTGTGTTCTCCGACCAAGATTGCAGAAATTGAGAGGCTTCAG 628      |
| QY                    | 657    | CA 658                                                              |
| DB                    | 629    | CA 630                                                              |

Search completed: February 2, 2003, 12:14:48  
Job time : 1745.09 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 2, 2003, 06:43:28 ; Search time 53.766 Seconds  
(without alignments)  
8013.329 Million cell updates/sec

Title: US-09-978-382A-5  
Perfect score: 959  
Sequence: 1 gaattcatcttccatctc.....ccaagagacggttacacaaa 959

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 396772 seqs, 224632407 residues

Total number of hits satisfying chosen parameters: 793544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA:\*

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3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*  
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11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
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13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID                  | Description       |
|------------|-------|-------------|--------|----|---------------------|-------------------|
| 1          | 959   | 100.0       | 959    | 9  | US-09-978-729A-5    | Sequence 5, Appli |
| 2          | 959   | 100.0       | 959    | 9  | US-09-981-087A-5    | Sequence 5, Appli |
| 3          | 959   | 100.0       | 959    | 9  | US-09-978-382A-5    | Sequence 5, Appli |
| 4          | 959   | 100.0       | 959    | 9  | US-09-978-740A-5    | Sequence 5, Appli |
| 5          | 959   | 100.0       | 959    | 10 | US-09-978-730-5     | Sequence 5, Appli |
| 6          | 536.8 | 56.0        | 896    | 9  | US-09-978-729A-3    | Sequence 3, Appli |
| 7          | 536.8 | 56.0        | 896    | 9  | US-09-981-087A-3    | Sequence 3, Appli |
| 8          | 536.8 | 56.0        | 896    | 9  | US-09-978-382A-3    | Sequence 3, Appli |
| 9          | 536.8 | 56.0        | 896    | 9  | US-09-978-740A-3    | Sequence 3, Appli |
| 10         | 536.8 | 56.0        | 896    | 10 | US-09-978-730-3     | Sequence 3, Appli |
| 11         | 186.2 | 19.4        | 845    | 10 | US-09-770-445-644   | Sequence 644, App |
| 12         | 152.2 | 15.9        | 645    | 9  | US-09-938-842A-1776 | Sequence 1776, Ap |
| 13         | 152.2 | 15.9        | 645    | 9  | US-09-853-450-33    | Sequence 33, Appl |
| 14         | 148.4 | 15.5        | 1062   | 9  | US-09-978-729A-1    | Sequence 1, Appli |
| 15         | 148.4 | 15.5        | 1062   | 9  | US-09-981-087A-1    | Sequence 1, Appli |
| 16         | 148.4 | 15.5        | 1062   | 9  | US-09-978-382A-1    | Sequence 1, Appli |
| 17         | 148.4 | 15.5        | 1062   | 9  | US-09-978-740A-1    | Sequence 1, Appli |
| 18         | 148.4 | 15.5        | 1062   | 10 | US-09-978-730-1     | Sequence 1, Appli |
| 19         | 144.6 | 15.1        | 1345   | 9  | US-09-853-450-7     | Sequence 7, Appli |

|    |       |      |      |    |                     |                   |
|----|-------|------|------|----|---------------------|-------------------|
| 20 | 142.2 | 14.8 | 1280 | 10 | US-09-970-624-1     | Sequence 1, Appli |
| 21 | 138.2 | 14.4 | 666  | 9  | US-09-938-842A-2442 | Sequence 2442, Ap |
| 22 | 132.8 | 13.8 | 753  | 9  | US-09-853-450-29    | Sequence 29, Appl |
| 23 | 128.8 | 13.4 | 5497 | 10 | US-09-916-780A-7    | Sequence 7, Appli |
| 24 | 126.6 | 13.2 | 747  | 9  | US-09-853-450-27    | Sequence 27, Appl |
| 25 | 125.6 | 13.1 | 794  | 9  | US-09-853-450-3     | Sequence 3, Appli |
| 26 | 124.4 | 13.0 | 705  | 9  | US-09-938-842A-2404 | Sequence 2404, Ap |
| 27 | 124   | 12.9 | 768  | 9  | US-09-853-450-5     | Sequence 5, Appli |
| 28 | 117.8 | 12.3 | 777  | 9  | US-09-938-842A-1873 | Sequence 1873, Ap |
| 29 | 117.6 | 12.3 | 663  | 9  | US-09-853-450-37    | Sequence 37, Appl |
| 30 | 115.2 | 12.0 | 779  | 9  | US-09-853-450-9     | Sequence 9, Appli |
| 31 | 115   | 12.0 | 1057 | 9  | US-09-853-450-1     | Sequence 1, Appli |
| 32 | 110   | 11.5 | 756  | 9  | US-09-853-450-11    | Sequence 11, Appl |
| 33 | 106.8 | 11.1 | 633  | 9  | US-09-853-450-35    | Sequence 35, Appl |
| 34 | 105.2 | 11.0 | 756  | 9  | US-09-938-842A-718  | Sequence 718, App |
| 35 | 104.6 | 10.9 | 633  | 9  | US-09-938-842A-1202 | Sequence 1202, Ap |
| 36 | 103   | 10.7 | 5131 | 9  | US-09-853-450-43    | Sequence 43, Appl |
| 37 | 101.4 | 10.6 | 5392 | 9  | US-09-853-450-45    | Sequence 45, Appl |
| 38 | 100.4 | 10.5 | 756  | 9  | US-09-853-450-13    | Sequence 13, Appl |
| 39 | 96.8  | 10.1 | 714  | 9  | US-09-853-450-31    | Sequence 31, Appl |
| 40 | 96.8  | 10.1 | 5070 | 9  | US-09-853-450-44    | Sequence 44, Appl |
| 41 | 95.8  | 10.0 | 262  | 10 | US-09-878-574-9686  | Sequence 9686, Ap |
| 42 | 95    | 9.9  | 5171 | 9  | US-09-853-450-42    | Sequence 42, Appl |
| 43 | 95    | 9.9  | 5483 | 9  | US-09-853-450-47    | Sequence 47, Appl |
| 44 | 92.2  | 9.6  | 407  | 10 | US-09-878-574-19    | Sequence 19, Appl |
| 45 | 91.2  | 9.5  | 365  | 10 | US-09-878-574-16    | Sequence 16, Appl |

#### ALIGNMENTS

##### RESULT 1

US-09-978-729A-5  
; Sequence 5, Application US/09978729A  
; Patent No. US20020178465A1

##### GENERAL INFORMATION:

; APPLICANT: Yanofsky, Martin F.  
; APPLICANT: Liljegen, Sarah  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 19452A-000950US  
; CURRENT APPLICATION NUMBER: US/09/978,729A  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: US 60/090,649  
; PRIOR FILING DATE: 1998-06-25  
; PRIOR APPLICATION NUMBER: US 09/339,998  
; PRIOR FILING DATE: 1999-06-25  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5

; LENGTH: 959

; TYPE: DNA

; ORGANISM: Arabidopsis sp.

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (78)..(818)

; OTHER INFORMATION: AGAMOUS-LIKE 5 (AGL5)

US-09-978-729A-5

Query Match 100.0%; Score 959; DB 9; Length 959;  
Best Local Similarity 100.0%; Pred. No. 2.3e-292;  
Matches 959; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCATCTCCCATCTCCTCTCTTTCTTTCTGATCATAATAATCTTGCTAAGCC 60  
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Db 1 GAATTCATCTCCCATCTCCTCTTTCTTTCTGATCATAATAATCTTGCTAAGCC 60  
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QY 61 AGCTAGGGCTTATAGAAATGGAGGGTGGTGGAGTAAATGAAGTAGCAGAGACGACGAAGA 120  
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Db 61 AGCTAGGGCTTATAGAAATGGAGGGTGGTGGAGTAAATGAAGTAGCAGAGACGACGAAGA 120  
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QY 121 AGATAGGGAGAGGGAAGATAGAGATAAGAGGATAGAGACACTACGAATCGTCAAGTCA 180

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Db 121 AGATAGGAGAGGGAAGATAGAGATAAGAGGATAGAGAACACTACGAATCGTCAAGTCA 180  
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Db 181 CTTTCTGCAACGACGCAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGTGTGTG 240  
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Db 720 AAGAAATCGAGTGTATACATCAAGGACAGTTTACGAGTCGGGTGTTACTTCTTCTCACC 780  
Qy 781 CCTCCAAACCAAGACCAACCACTCTGCAACTTGTGATTGATTCAGTCTAACATAAGCTTCTT 840  
Db 781 CCTCCAAACCAAGACCAACCACTCTGCAACTTGTGATTGATTCAGTCTAACATAAGCTTCTT 840

RESULT 2  
US-09-981-087A-5  
; Sequence 5, Application US/09981087A  
; Patent No. US20020178466A1  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin F.  
; APPLICANT: Liljgren, Sarah  
; APPLICANT: Farrandiz, Cristina  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 19452A-000940US  
; CURRENT APPLICATION NUMBER: US/09/981,087A  
; CURRENT FILING DATE: 2002-05-21  
; PRIOR APPLICATION NUMBER: US 60/090,649  
; PRIOR FILING DATE: 1998-06-25  
; PRIOR APPLICATION NUMBER: US 09/339,998

; PRIOR FILING DATE: 1999-06-25  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 959  
; TYPE: DNA  
; ORGANISM: Arabidopsis sp.  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (78)..(818)  
; OTHER INFORMATION: AGAMOUS-LIKE 5 (AGL5)  
US-09-981-087A-5

Query Match 100.0%; Score 959; DB 9; Length 959;  
Best Local Similarity 100.0%; Pred. No. 2.3e-292;  
Matches 959; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAATTTCATCTTCCCATCCCTCACTTCTCTTTCTGTATCATTAATCTTGTAAAGCC 60  
Db 1 GAATTTCATCTTCCCATCCCTCACTTCTCTTTCTGTATCATTAATCTTGTAAAGCC 60  
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Qy 121 AGATAGGAGAGGGAAGATAGAGATAAGAGGATAGAGAACACTACGAATCGTCAAGTCA 180  
Db 121 AGATAGGAGAGGGAAGATAGAGATAAGAGGATAGAGAACACTACGAATCGTCAAGTCA 180  
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Db 181 CTTTCTGCAAAACGACGCAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGTGTGTG 240  
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Db 241 ACGTGAAGTTGCTCTTGTTCATCTTCTCCACTCGAGGCGTCTTACGAGTACGCCAACA 300  
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Db 301 ACAGTGTGAGAGGAACAATAGAAAGGTACAAGAAAGCTTGTCTCCGACGCCGTTAACCCCTC 360  
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Db 361 CGACCATCACCGAAGCTAATFACTAGTACTATACGAAGAGGCGTCTAAACTCCGGAGAC 420  
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Db 601 TGCAAAACGATAAATGATGTATCTCCGCTCCAGATTACTGAAAGAACAGGCTCTACAGCAAC 660  
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Db 661 AAGAAATCGAGTGTATACATCAAGGACAGTTTACGAGTCGGGTGTTACTTCTTCTCACC 720  
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Db 721 AGTCGGGCGAGTATACCGGAATTTATTCGGTTAAACCTTCTTGAACCGAATCAGAAT 780  
Qy 781 CCTCCAAACCAAGACCAACCACTCTGCAACTTGTGATTGATTCAGTCTAACATAAGCTTCTT 840  
Db 781 CCTCCAAACCAAGACCAACCACTCTGCAACTTGTGATTGATTCAGTCTAACATAAGCTTCTT 840

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QY 841 TCCTCAGCCTGAGATCGATCTATAGTGTACCTAAATGCGGCCCGGTCCCTCAACATCTA 900
Db 841 TCCTCAGCCTGAGATCGATCTATAGTGTACCTAAATGCGGCCCGGTCCCTCAACATCTA 900
QY 901 GTCCGAAGCTGAGGGGAACCACTAGTGTATACGAAACCTCCAAAGAGACGGTTACACAAA 959
Db 901 GTCCGAAGCTGAGGGGAACCACTAGTGTATACGAAACCTCCAAAGAGACGGTTACACAAA 959

RESULT 3
US-09-978-382A-5
; Sequence 5, Application US/09978382A
; Publication No. US20020194647A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegren, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; FILE OF INVENTION: Plants
; FILE REFERENCE: 19452A-000930US
; CURRENT APPLICATION NUMBER: US/09/978, 382A
; PRIOR FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/090, 649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339, 998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 959
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (78)..(818)
; OTHER INFORMATION: AGAMOUS-LIKE 5 (AGL5)
US-09-978-382A-5

Query Match 100.0%; Score 959; DB 9; Length 959;
Best Local Similarity 100.0%; Pred. No. 2.3e-292;
Matches 959; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCATCTCCCATCCTCACTTCTCTTCTCTGATCATAAATTAATCTGTAAAGCC 60
Db 1 GAATTCATCTCCCATCCTCACTTCTCTTCTCTGATCATAAATTAATCTGTAAAGCC 60
QY 61 AGCTAGGGCTTATAGAAATGAGGGTGGTGGCAGTAATGAAGTAGCAGAGACGACGAAGA 120
Db 61 AGCTAGGGCTTATAGAAATGAGGGTGGTGGCAGTAATGAAGTAGCAGAGACGACGAAGA 120
QY 121 AGATAGGAGAGGGAAGATAGAGATAAGAGGATAGAGAACACTACGAATCGTCAAGTCA 180
Db 121 AGATAGGAGAGGGAAGATAGAGATAAGAGGATAGAGAACACTACGAATCGTCAAGTCA 180
QY 181 CTTTCTGCAACGACGCAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGTCTTGTGTG 240
Db 181 CTTTCTGCAACGACGCAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGTCTTGTGTG 240
QY 241 ACGCTGAGGTTGCTCTTGTCTATCTTCTCCACTCGAGCGCGTCTCTACGAGTACGCCAACA 300
Db 241 ACGCTGAGGTTGCTCTTGTCTATCTTCTCCACTCGAGCGCGTCTCTACGAGTACGCCAACA 300
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Db 301 ACAGTGTGAGAGGAACAATAGAAAGGTACAGAAAGCTTGTCCGAGCGCGTTAAACCCCTC 360
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Db 361 CGACCATCAGGAAGTAATCTACTACTATCAGCAAGAGCGGTCTAAACTCCGGAGAC 420
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Db 541 CCAAGAACGACGAGATGTTAGTTGCAGAGATTGAATACATGCAAAAAAGGGAATCCGAGC 600
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RESULT 4
US-09-978-740A-5
; Sequence 5, Application US/09978740A
; Publication No. US20030005481A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegren, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; FILE OF INVENTION: Plants
; FILE REFERENCE: 19452A-000960US
; CURRENT APPLICATION NUMBER: US/09/978, 740A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/090, 649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339, 998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 959
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (78)..(818)
; OTHER INFORMATION: AGAMOUS-LIKE 5 (AGL5)
US-09-978-740A-5

Query Match 100.0%; Score 959; DB 9; Length 959;
Best Local Similarity 100.0%; Pred. No. 2.3e-292;
Matches 959; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCATCTTCCCATCCTCACTTCTTCTTCTTCTTCTGATCATAAATTAATCTGTAAAGCC 60
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RESULT 5  
US-09-978-730-5  
; Sequence 5, Application US/09978730  
; Patent No. US20020129403A1  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin F.  
; APPLICANT: Liljefgren, Sarah  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 19452A-00092005  
; CURRENT APPLICATION NUMBER: US/09/978,730  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: US 60/090,649

; PRIOR FILING DATE: 1998-06-25  
; PRIOR APPLICATION NUMBER: US 09/339,998  
; PRIOR FILING DATE: 1999-06-25  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 959  
; TYPE: DNA  
; ORGANISM: Arabidopsis sp.  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (78)..(818)  
; OTHER INFORMATION: AGAMOUS-LIKE 5 (AGL5)  
US-09-978-730-5

Query Match 100.0%; Score 959; DB 10; Length 959;  
Best Local Similarity 100.0%; Pred. No. 2.3e-292;  
Matches 959; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAATTCATCTCCATCCCTCATTCTCTTTCTTCTGTATCATTAATTAATCTTGGTAAGCC 60  
Db 1 GAATTCATCTCCATCCCTCATTCTCTTTCTTCTGTATCATTAATTAATCTTGGTAAGCC 60  
Qy 61 AGTAGGGCTTATAGAAATGGAGGTGGTGGAGTAATGAAGTAGCAGAGACGACAGA 120  
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RESULT 6

US-09-978-729A-3

; Sequence 3, Application US/09978729A

; Patent No. US20020178465A1

; GENERAL INFORMATION:

; APPLICANT: Yanofsky, Martin F.

; APPLICANT: Liljegren, Sarah

; APPLICANT: Farrandiz, Cristina

; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 19452A-000950US

; CURRENT APPLICATION NUMBER: US/09/978,729A

; CURRENT FILING DATE: 2002-06-10

; PRIOR FILING DATE: 1998-06-25

; PRIOR APPLICATION NUMBER: US 60/090,649

; PRIOR FILING DATE: 1999-06-25

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3

; LENGTH: 896

; TYPE: DNA

; ORGANISM: Arabidopsis sp.

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (7)..(753)

; OTHER INFORMATION: AGAMOUS-LIKE 1 (AGL1)

US-09-978-729A-3

Query Match 56.0%; Score 536.8; DB 9; Length 896;

Best Local Similarity 82.1%; Pred. No. 3.4e-159;

Matches 632; Conservative 0; Mismatches 132; Indels 6; Gaps 1;

QY 77 AATGGAGGGTGGTGGAGTAATGAGTACGAGAGCAGCAGCAAGAAAGATAGGAGGGAA 136

Db 6 AATGGAGGAAGGTGGGAGTAGTCACGCGCAGAGACTAGCAAGAACTAGGAGGGAA 65

QY 137 GATAGAGATAAAGAGATAGAGAACACTAGCAATCGTCAAGTCACTTTCTGCAAAACGACG 196

Db 66 AATAGAGATAAAGAGATAGAGAACACAACAATCGTCAAGTCACTTTCTGCAAAACGACG 125

QY 197 CAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGTGTGAGCGCTGAGGTTGCTCT 256

Db 126 CAATGGTCTTCTCAAGAAAGCTTATGAACTCTCTGTGTGATGCGGAAGTTGCCCT 185

QY 257 TGTATCTTCTCAGAAAGCTTATGAGTACGAGAGCAGCAAGAAAGATAGGAGGGAA 316

Db 246 AATTGAAAGGTACAGAAAGCTTGTCCGATGCCCTCAACCTCTTCCGTCACCGAAGC 305

QY 377 TAATCTAGTACTATCAGCAAGAGCGTCTAACTCCGAGAGACAGATTCGGGACATTTCA 436

Db 306 TAATCTAGTACTATCAGCAAGAGCGCTTAAGCTTCGAGGAGAGATTCGAGATATTCA 365

QY 437 GAATTTGAACACACATTTCTTGGTGAATCTCTTGGTTCCTTGAATTTAAGGAACTCAA 496

Db 366 GAATTTCAAATAGGCATATTTGTTGGGGAATCACTTGGTTCCTTGAATTTAAGGAACTCAA 425

QY 497 GAACCTTGAAAGTAGGCTTGAGAAAGGAATCAGTCGTGTCCTCGATCCAAAGAACGAGAT 556

Db 426 AAACCTAGAGGACGCTCTTGAATAAGAAATCAGCCGTGTCGCTCCAAAAAGAAATGAGCT 485

QY 557 GTTAGTTCAGAGATTGAATATACATGCAAAAAGGGAATCGAGCTGCAAAACGATACAT 516

Db 486 GTTAGTGGCAGAGATAGAGTATATGCAAGAGGGAATGAGTTGCAACACAATAACAT 545

QY 617 GTATCTCCGCTCCAAGATTACTGAA-----AGAACAGGTTCTACAGCAACAAGAAATCGAG 670

Db 546 GTACCTGCGAGCAAGATAGCCGAGCGGCGAGATTGAATCCGGACCAGCAGGAATCGAG 605

QY 671 TGTGATACATCAAGGACAGTTTACGAGTCGGGTGTTACTTCTTCTACACCAGTCGGGGCA 730

Db 606 TGTGATACAAGGACGACAGTTTACGAATCCGGTGTATCTTCTCATGACCAGTCGGAGCA 665

QY 731 GTATAACCGGAATTATATTCGGGTTAACCTTCTTGAACCGGAATCAGAATTCCTTCCAAACCA 790

Db 666 TTATATCGGAACATATATTCGGGTGAACCTTCTTGAACCGGAATCAGAATTCCTTCCGGCCA 725

QY 791 AGACCAACCACTCTGCAACTTGTGTTGATTCAGTCTTAACATAAGCTTCTT 840

Db 726 AGACCAACCTCTCTCTCAACTTGTGTTGATTCAGTCTTAACATAAGCTTCTT 775

RESULT 7

US-09-981-087A-3

; Sequence 3, Application US/09981087A

; Patent No. US20020178466A1

; GENERAL INFORMATION:

; APPLICANT: Yanofsky, Martin F.

; APPLICANT: Liljegren, Sarah

; APPLICANT: Farrandiz, Cristina

; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 19452A-000940US

; CURRENT APPLICATION NUMBER: US/09/981,087A

; CURRENT FILING DATE: 2002-05-21

; PRIOR FILING DATE: 1998-06-25

; PRIOR APPLICATION NUMBER: US 60/090,649

; PRIOR FILING DATE: 1999-06-25

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3

; LENGTH: 896

; TYPE: DNA

; ORGANISM: Arabidopsis sp.

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (7)..(753)

; OTHER INFORMATION: AGAMOUS-LIKE 1 (AGL1)

US-09-981-087A-3

Query Match 56.0%; Score 536.8; DB 9; Length 896;

Best Local Similarity 82.1%; Pred. No. 3.4e-159;

Matches 632; Conservative 0; Mismatches 132; Indels 6; Gaps 1;

QY 77 AATGGAGGGTGGTGGAGTAATGAGTACGAGAGCAGCAGCAAGAAAGATAGGAGGGAA 136

Db 6 AATGGAGGAAGGTGGGAGTAGTCACGCGCAGAGACTAGCAAGAACTAGGAGGGAA 65

QY 137 GATAGAGATAAAGAGATAGAGAACACTAGCAATCGTCAAGTCACTTTCTGCAAAACGACG 196

Db 66 AATAGAGATAAAGAGATAGAGAACACAACAATCGTCAAGTCACTTTCTGCAAAACGACG 125

QY 197 CAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGTGTGAGCGCTGAGGTTGCTCT 256

Db 126 CAATGGTCTTCTCAAGAAAGCTTATGAACTCTCTGTGTGATGCGGAAGTTGCCCT 185

QY 257 TGTATCTTCTCAGAAAGCTTATGAGTACGAGAGCAGCAAGAAAGATAGGAGGGAA 316

Db 186 CGTCATCTTCTCCACTCGTGGCGCTCTCTATGAGTACGCCCAACAACAGTGTGAGGGGTAC 245



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; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(753)
; OTHER INFORMATION: AGAMOUS-LIKE 1 (AGL1)
US-09-978-740A-3

Query Match          56.0%; Score 536.8; DB 9; Length 896;
Best Local Similarity 82.1%; Pred. No. 3.4e-159;
Matches 632; Conservative 0; Mismatches 132; Indels 6; Gaps 1;

QY 77 AATGGAGGTGGTGGAGTAAAGTAGCAGAGAGCAGCAAGAAAGATAGGGAGGGAA 136
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Db 6 AATGGAGGAAGGTGGAGTAGTCACGACGAGAGTAGCAAGAACTAGGGAGGGAA 65

QY 137 GATAGAGATAAAGAGGATAGAGAACTACGAAATCGTCAAGTCACCTTCTGCAACGACG 196
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Db 66 AATAGAGATAAAGAGGATAGAGAACACAAATCGTCAAGTACTTTCTGCAACGACG 125

QY 197 CAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGTCTGTGTGACGCTGAGTTGCTCT 256
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Db 126 CAATGGTCTTCTCAAGAAAGCTTATGAACCTCTCTGTCTGTGTGATGCCGAAGTTGCCCT 185

QY 257 TGTCACTCTCCACTCGAGCGCTCTCTAGGAGTACGCCAACACACAGTGTGAGAGGAAC 316
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Db 186 CGTCATCTTCTCCACTCGTGGCGCTCTATGATACGCCAACACACAGTGTGAGGGGTAC 245

QY 317 AATAGAAAGGTACAGAAAGCTTGCTCCGACGCCGTTAAACCTCCGACCATCACCCGAAGC 376
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Db 246 AATTGAAGGTACAGAAAGCTTGTTCGGATGCCGTCAACCTCTCCGTCAACCGAAGC 305

QY 377 TAATACTCAGTACTATCAGCAAGAGCGTCTAAACTCCGGAGACAGATTCCGGGACATTCA 436
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Db 306 TAATACTCAGTACTATCAGCAAGAGCGCTTAAGCTTCGGAGGCGAGATTCCGAGATATCA 365

QY 437 GAATTTGAACAGACACATCTTGGTGAATCTCTTGGTTCCTTGAACCTTTAAGGAACCTCAA 496
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Db 366 GAATTTCAAATAGGCATATTGTTGGGGAATCACTTGGTTCCTTGAACCTTCAAGGAACCTCAA 425

QY 497 GAACCTTGAAGTAGGCTTGAGAAAGGAATCAGTCGTGTCCGATCCAAAGACGACGAGAT 556
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Db 426 AAACCTTAGAAGGACGCTCTTGAAGAAAGGAATCAGCGGTGTCGGCTCCAAAGAAATGAGCT 485

QY 557 GTTAGTTGCAGAGATTGAATACATGCAAAAAGGAAATCGAGTGCAGGAGGAAATCAACAT 616
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 486 GTTAGTGGCAGATAGATATATGCAGAGAGGAAATGAGGATTGCAACACAATTAACAT 545

QY 617 GTATCTCCGCTCCAAAGATTACTGAA-----AGAACAGGTCTACAGCAACAAGATCGAG 670
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 546 GTACCTCGCAGCAAGATAGCCGAGGCGCCAGATTGAATCCGACGAGGAGATTCGAG 605

QY 671 TGTGATACATCAAGGACAGTTTACGAGTCCGGGTGTTACTTCTTCAACCATCGGGGCA 730
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Db 606 TGTGATACAAAGGACGACAGTTTACGAATCCGGTGATCTTCTCATGACCGAGTCGAGCA 665

QY 731 GTATAACCGGAATTATATTCGGTTAACCTTCTTGACCGGAATCAGAATTCTCTCCAAACCA 790
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 666 TTATAATCGGAACCTATATTCGGGTGACCTTCTTGAAACCGGAATCAGCAATTCTCCGGCCA 725

QY 791 AGACCAACCACTCTGCAACTTGTGTGATTGAGTCTAAACATTAAGCTTCTT 840
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Db 726 AGACCAACCTCTCTTCAACTTGTGTAACCTCAAAAACATGATAAATTGTTT 775

RESULT 10
US-09-978-730-3
; Sequence 3, Application US/09978730
; Patent No. US20020129403A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljgren, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
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; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-0009200S
; CURRENT APPLICATION NUMBER: US/09/978,730
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 896
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(753)
; OTHER INFORMATION: AGAMOUS-LIKE 1 (AGL1)
US-09-978-730-3

Query Match          56.0%; Score 536.8; DB 10; Length 896;
Best Local Similarity 82.1%; Pred. No. 3.4e-159;
Matches 632; Conservative 0; Mismatches 132; Indels 6; Gaps 1;

QY 77 AATGGAGGTGGTGGAGTAAAGTAGCAGAGAGCAGCAAGAAAGATAGGGAGGGAA 136
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6 AATGGAGGAAGGTGGAGTAGTCACGACGAGAGTAGCAAGAACTAGGGAGGGAA 65

QY 137 GATAGAGATAAAGAGGATAGAGAACTACGAAATCGTCAAGTCACCTTCTGCAACGACG 196
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Db 66 AATAGAGATAAAGAGGATAGAGAACACAAATCGTCAAGTACTTTCTGCAACGACG 125

QY 197 CAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGTCTGTGTGACGCTGAGTTGCTCT 256
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 126 CAATGGTCTTCTCAAGAAAGCTTATGAACCTCTCTGTCTGTGTGATGCCGAAGTTGCCCT 185

QY 257 TGTCACTCTCCACTCGAGCGCTCTCTAGGAGTACGCCAACACACAGTGTGAGAGGAAC 316
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Db 186 CGTCATCTTCTCCACTCGTGGCGCTCTATGATACGCCAACACACAGTGTGAGGGGTAC 245

QY 317 AATAGAAAGGTACAGAAAGCTTGCTCCGACGCCGTTAAACCTCCGACCATCACCCGAAGC 376
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Db 246 AATTGAAGGTACAGAAAGCTTGTTCGGATGCCGTCAACCTCTCCGTCAACCGAAGC 305

QY 377 TAATACTCAGTACTATCAGCAAGAGCGTCTAAACTCCGGAGACAGATTCCGGGACATTCA 436
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Db 306 TAATACTCAGTACTATCAGCAAGAGCGCTTAAGCTTCGGAGGCGAGATTCCGAGATATCA 365

QY 437 GAATTTGAACAGACACATCTTGGTGAATCTCTTGGTTCCTTGAACCTTTAAGGAACCTCAA 496
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Db 366 GAATTTCAAATAGGCATATTGTTGGGGAATCACTTGGTTCCTTGAACCTTCAAGGAACCTCAA 425

QY 497 GAACCTTGAAGTAGGCTTGAGAAAGGAATCAGTCGTGTCCGATCCAAAGACGACGAGAT 556
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Db 426 AAACCTTAGAAGGACGCTCTTGAAGAAAGGAATCAGCGGTGTCGGCTCCAAAGAAATGAGCT 485

QY 557 GTTAGTTGCAGAGATTGAATACATGCAAAAAGGAAATCGAGTGCAGGAGGAAATCAACAT 616
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Db 486 GTTAGTGGCAGATAGATATATGCAGAGAGGAAATGAGGATTGCAACACAATTAACAT 545

QY 617 GTATCTCCGCTCCAAAGATTACTGAA-----AGAACAGGTCTACAGCAACAAGATCGAG 670
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 546 GTACCTCGCAGCAAGATAGCCGAGGCGCCAGATTGAATCCGACGAGGAGATTCGAG 605

QY 671 TGTGATACATCAAGGACAGTTTACGAGTCCGGGTGTTACTTCTTCAACCATCGGGGCA 730
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 606 TGTGATACAAAGGACGACAGTTTACGAATCCGGTGATCTTCTCATGACCGAGTCGAGCA 665

QY 731 GTATAACCGGAATTATATTCGGTTAACCTTCTTGACCGGAATCAGAATTCTCTCCAAACCA 790
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Db 666 TTATAATCGGAACCTATATTCGGGTGACCTTCTTGAAACCGGAATCAGCAATTCTCCGGCCA 725

QY 791 AGACCAACCACTCTGCAACTTGTGTGATTGAGTCTAAACATTAAGCTTCTT 840
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Db 726 AGACCAACCTCTCTTCAACTTGTGTAACCTCAAAAACATGATAAATTGTTT 775
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Db 726 AGACCAACCCCTCTTCAACTGTGTAACTCAAAACATGATAACTTGTT 775

RESULT 11

US-09-770-445-644/C

; Sequence 644, Application US/09770445

; Patent No. US2002023281A1

; GENERAL INFORMATION:

; APPLICANT: Gorlach, Jörn

; APPLICANT: An, Yong-Qiang

; APPLICANT: Hamilton, Carol M.

; APPLICANT: Price, Jennifer L.

; APPLICANT: Raines, Tracy M.

; APPLICANT: Yu, Yang

; APPLICANT: Rameaka, Joshua G.

; APPLICANT: Page, Amy

; APPLICANT: Matthew, Abraham V.

; APPLICANT: Ledford, Brooke L.

; APPLICANT: Woessner, Jeffrey P.

; APPLICANT: Haas, William David

; APPLICANT: Garcia, Carlos A.

; APPLICANT: Krickler, Maja

; APPLICANT: Slader, Ted

; APPLICANT: Davis, Keith R.

; APPLICANT: Allen, Keith

; APPLICANT: Hoffman, Neil

; APPLICANT: Hurban, Patrick

; TITLE OF INVENTION: Expressed Sequences of Arabidopsis

; FILE REFERENCE: 2023US (PARA-012PRV)

; CURRENT APPLICATION NUMBER: US/09/770,445

; CURRENT FILING DATE: 2001-01-26

; PRIOR APPLICATION NUMBER: US 60/178,472

; PRIOR FILING DATE: 2000-01-27

; NUMBER OF SEQ ID NOS: 999

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 644

; LENGTH: 845

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

US-09-770-445-644

Query Match 19.4%; Score 186.2; DB 10; Length 845;

Best Local Similarity 65.5%; Pred. No. 1.3e-48;

Matches 272; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

QY 247 AGGTTGCTTGTCTATCTTCCACTCGAGCCGCTCTACGAGTACGCCAACACAGTG 306

Db 845 AGTTGGCTCATTTGTTTCTCCACTCGTGGCCGCTCTATGAATACGCCAATAACA 786

QY 307 TGAGGGAACAATAAGAGGTACAAGAAAGCTTGCTCCGAGCCCGTTAACCCCTCCGACCA 366

Db 785 TAAGATCAACCATTTGAGAGGTACAAGAAAGCTTGTTCTGATAGCACCACACTAGCACTG 726

QY 367 TCACCGAGCTAATCTACGTAATCTACGAAAGAGGCGTCTAAACTCCGGAGACAGATTC 426

Db 725 TCCAAGAAATCAATGCGCGCTACTATCAACAAGAATCTGTAAGCTTGAGACAACAGATCC 666

QY 427 GGGACATTCAGAAATTTGAACAGACACATCTTGGTGAATCTCTTGGTTCCTTGAACCTTA 486

Db 665 AAACGATTCAAAACTCCAACAGGAATCTGATGGGAGACTCTTTAGTTCCTTAAGTGTC 606

QY 487 AGGAATCAAGAACCTTTGAAGAGTGTGAGAAAGGAATCAGTCGTGTCGATCCAAGA 546

Db 605 AGGAATCAAAACAGTTGAGATCGCTTGAGAAAGCTATCTTAGGATCAGGTCCAAGA 546

QY 547 AGCAGGAGATGTTAGTTGCAGAGATTGAATACATGCAAAAAGGGAATCGAGCTGCAAA 606

Db 545 AGCATGAGTTGCTTTTAGTTGAATCGAAACCCGCGCAGAAAGGGAGATTGAGCTTGACA 486

QY 607 AGGATAACATGTATCTCCGCTCCAAGATTACTGAAAGAACAGAGTCTACAGCAACA 661

Db 485 ATGAGAACATCTATCTTAAGAACTAAGGTAGCAGAAGTGGAGAGGTATCAACAACA 431

RESULT 12

US-09-938-842A-1776

; Sequence 1776, Application US/09938842A

; Patent No. US20020160378A1

; GENERAL INFORMATION:

; APPLICANT: Harper, Jeff

; APPLICANT: Kreps, Joel

; APPLICANT: Wang, Xun

; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

; FILE REFERENCE: SAME, AND METHODS OF USE

; CURRENT APPLICATION NUMBER: US/09/938,842A

; CURRENT FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: US 60/227,866

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: US 60/264,647

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/300,111

; NUMBER OF SEQ ID NOS: 5379

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

US-09-938-842A-1776

Query Match 15.9%; Score 152.2; DB 9; Length 645;

Best Local Similarity 56.5%; Pred. No. 5.7e-38;

Matches 283; Conservative 0; Mismatches 218; Indels 0; Gaps 0;

QY 123 ATAGGGAGAGGGGAAGATAGAGATAAAGAGGATAGAGACACTACGAAATCGTCAAGTCACT 182

Db 1 ATGGTCAGGGGCAAACTCAGATGAAGAAATAGAGAAATGCAACAAGCAGACAAGTGACT 60

QY 183 TTCTGCAACGACGCAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTCTTCTGTGTGAC 242

Db 61 TTCTCCAAAAGAGGAATGGTTTGTGAAGAAAGCCTTTGAGCTCTCAGTGTCTTGTGAT 120

QY 243 GCTGAGGTTGCTCTTGTCTATCTTCTCCACTCGAGGCGGCTCTCTAGGAGTACGCCAACAC 302

Db 121 GCTGAGTTTCTCTTATCATCTTCTCTCTCTAAAGCAGCAACTTTTATGAATTCGCCAGCTCC 180

QY 303 AGTGTGAGAGGAACAATAAGAAAGGTACAAAGAGCTTGCTCCGAGCCCGTTAACCCCTCCG 362

Db 181 AATATGCAAGATACCATAGATCGTTTATCTGAGGCATACATAAGGATCGAGTCAGCACCAAA 240

QY 363 ACCATCACCGAAGCTAATACTCAGTACTATCAGCAAGAGGCGTCTAAACTCCGGAGACAG 422

Db 241 CCGGTTTCTGAAGAAATATGCAGCATTTTGAATATGAGCAGCAAAACATGATGAAGAAA 300

QY 423 ATTGGGACATTCAGAAATTTGAACAGACACATCTTCTGGTGAATCTCTTGGTTCCTTGAAC 482

Db 301 ATTGAACAACCTCGAAGCTTCTAAACGTAACACTCTTGGGAGAAAGGCATAGGAACATGCTCA 360

QY 483 TTTAAGGAATCAAGAACCTTTGAAAGTAGGCTTGAGAAAGGAATCAGTCGTGTCCGATCC 542

Db 361 ATCGAGGAGCTGCAACAGATTGAGCAACAGCTTGAGAAAGAGTGTCAAATGTATTTCGAGCA 420

QY 543 AAGAAGCACGAGATGTAGTTGCAGAGATTGAATACATGCAAAAAGGGAATTCAGAGCTG 602

Db 421 AGAAGACTCAAGTGTTTAAGGAACAATTTGAGCAGCTCAAGCAAAAGGAGAAAGCTCTA 480

QY 603 CAAAACGATACATGTATCTC 623

Db 481 GCTGCAGAAACAGAGAAGCTC 501

RESULT 13

US-09-853-450-33

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; Sequence 33, Application US/09853450
; Publication No. US20020194645A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Pelaz, Soraya
; APPLICANT: Ditta, Gary
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; TITLE OF INVENTION: Exhibiting Modulated Reproductive Development
; FILE REFERENCE: 19452A-002400US
; CURRENT APPLICATION NUMBER: US/09/853,450
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(645)
; OTHER INFORMATION: AGL20 (SUPPRESSOR OF CONSTANS (CO) OVEREXPRESSION
; OTHER INFORMATION: 1 (SOCL))
US-09-853-450-33

Query Match 15.9%; Score 152.2; DB 9; Length 645;
Best Local Similarity 56.5%; Pred. No. 5.7e-38;
Matches 283; Conservative 0; Mismatches 218; Indels 0; Gaps 0;

QY 123 ATAGGGAGAGGAGATAGAGATAAAGAGGATAGAGAACACTAGCAATCGTCAAGTCACT 182
Db 1 ATGGTGAGGGGCAAACTCAGATGAGAGATAGAGATGCAACAGACAGCAAGTCACT 60

QY 183 TTCTGTCAACAGCGCAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGCTGTGTGAC 242
Db 61 TTCTCCAAAAGAGGAATGGTTGTGTAAGAAAGCCCTTTGAGCTCTCAGTGTGTGAT 120

QY 243 GGTGAGGTGCTCTGTGTCATCTCTCCACTCGAGGCCCTCTCTACGAGTACGCCAACAC 302
Db 121 GCTGAAGTTTCTTATCATCTCTCTCTAAAGGCAAACTTTATGAATTCGCCAGCTCC 180

QY 303 AGTGTGAGAGGACAAATAGAAAGGTACAAGAAAGCTTGCTCCGACGCCGTTAACCCCTCG 362
Db 181 AATATGAAGATACCATAGATCGTTATCTGAGGCATCTAAGGATCGAGTCAGCACCCAAA 240

QY 363 ACATACCGAGCTAATCTCAGTACTATCAAGAGCGGCTCTAACTCCGGAGACAG 422
Db 241 CCGGTTTCTGAAGAAATATGAGCATTTGAATATGAAGCAGCAACATGATGAAGAAA 300

QY 423 ATTGGGACATTCAGAAATTTGAACAGACACATCTTGGTGAATCTCTTGGTTCTTGAAC 482
Db 301 ATTGAACAACCTCGAAGCTTCTAAACGTAACCTTTGGGAGAGGCATAGGAACATGCTCA 360

QY 483 TTTAAGGAACCTCAAGAACCTTGAAAGTAGGCTTGAGAAAGGATCAGTCGTGTCGATCC 542
Db 361 ATCGAGGAGCTCAACAGATGAGCAACAGCTTGAGAAAAGTCAAAATGATTCGAGCA 420

QY 543 AAGAACGACGAGATGTTAGTTCAGAGATTGAATACATGCAAAAAGGGAAATCGAGCTG 602
Db 421 AGAAGACTCAAGTGTTTAAGGAACAATTTGAGCAGCTCAGCAAAAGGAGAAAGCTCTA 480

QY 603 CAAAACGATAACATGTATCTC 623
Db 481 GCTGCAGAAAACGAGAAGCTC 501

RESULT 14
US-09-978-729A-1
; Sequence 1, Application US/09978729A
; Patent No. US20020178465A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegren, Sarah
```

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; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; FILE REFERENCE: 19452A-000950US
; CURRENT APPLICATION NUMBER: US/09/978,729A
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(829)
; OTHER INFORMATION: AGAMOUS-LIKE 8 (AGL8)
US-09-978-729A-1

Query Match 15.5%; Score 148.4; DB 9; Length 1062;
Best Local Similarity 56.5%; Pred. No. 1.2e-36;
Matches 297; Conservative 0; Mismatches 226; Indels 3; Gaps 1;

QY 121 AGATAGGGAGAGGAGATAGAGATAAAGAGATAGAGAACTACGAAATCGTCAAGTCA 180
Db 99 ATATGGGAAGAGGTAGGGTTTCAGCTGAGAGAGATAGAGAACAGATCAATAGCAAGTTA 158

QY 181 CTTTCTCAACAGCACGCAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGTCTGTGTG 240
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QY 478 TGAACCTTAAAGGAACCTCAAGAACCTTGAAGTAGGCTTGAGAAAGGAATCAGTCGTGTC 537
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RESULT 15
US-09-981-087A-1
; Sequence 1, Application US/09981087A
; Patent No. US20020178466A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegren, Sarah
; APPLICANT: Farrandiz, Cristina
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
```

; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 19452A-000940US  
; CURRENT APPLICATION NUMBER: US/09/981,087A  
; CURRENT FILING DATE: 2002-05-21  
; PRIOR APPLICATION NUMBER: US 60/090,649  
; PRIOR FILING DATE: 1998-06-25  
; PRIOR APPLICATION NUMBER: US 09/339,998  
; PRIOR FILING DATE: 1999-06-25  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1062  
; TYPE: DNA  
; ORGANISM: Arabidopsis sp.  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (101)..(829)  
; OTHER INFORMATION: AGAMOUS-LIKE 8 (AGL8)  
US-09-981-087A-1

|    | Query Match           | 15.5%;                                                       | Score 148.4;       | DB 9;           | Length 1062;      |
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|    | Best Local Similarity | 56.5%;                                                       | Pred. No. 1.2e-36; |                 |                   |
|    | Matches 297;          | Conservative                                                 | 0;                 | Mismatches 226; | Indels 3; Gaps 1; |
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Job time : 58.766 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 2, 2003, 06:06:04 ; Search time 46.0113 Seconds  
(without alignments)  
6391.971 Million cell updates/sec

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Perfect score: 959  
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Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | % Match | Query Length | DB ID | Description       |
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| 14         | 273.2 | 28.5    | 1457         | 1     | US-08-460-512-1   |
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| 16         | 188   | 19.6    | 5622         | 4     | US-09-349-677-3   |
| 17         | 150.4 | 15.7    | 498          | 4     | US-09-073-587-6   |
| 18         | 148.4 | 15.5    | 1062         | 4     | US-09-067-800-1   |
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| 21         | 147.6 | 15.4    | 1043         | 2     | US-08-867-087B-12 |
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| 27         | 144.6 | 15.1    | 1345         | 4     | US-09-398-326-7   |

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## ALIGNMENTS

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US-09-067-800-7  
; Sequence 7, Application US/09067800  
; Patent No. 6198024  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin P.  
; TITLE OF INVENTION: Seed Plants Characterized by Delayed  
; TITLE OF INVENTION: Seed Dispersal  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/067,800  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UD 2948  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 959 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 78..818  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: 1..959  
; OTHER INFORMATION: /note= "AGL5 cDNA and deduced  
; OTHER INFORMATION: protein sequences."  
US-09-067-800-7





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RESULT 3

US-09-067-800-5  
; Sequence 5, Application US/09067800  
; Patent No. 6198024  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin F.  
; APPLICANT: Ferrandiz, Cristina  
; TITLE OF INVENTION: Seed Plants Characterized by Delayed  
; TITLE OF INVENTION: Seed Dispersal  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/067,800  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.

; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UD 2948  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 896 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 7..753  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 896  
; OTHER INFORMATION: /note= "There is a poly(A) tail at  
; OTHER INFORMATION: the end of the CDNA sequence."  
; NAME/KEY: misc\_feature  
; LOCATION: 1..896  
; OTHER INFORMATION: /note= "AGL1 CDNA and deduced  
; OTHER INFORMATION: protein sequences."  
; US-09-067-800-5

Query Match 56.0%; Score 536.8; DB 4; Length 896;  
Best Local Similarity 82.1%; Pred. No. 4.6e-175;  
Matches 632; Conservative 0; Mismatches 132; Indels 6; Gaps 1;

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RESULT 4  
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; Sequence 5, Application US/09349677  
; Patent No. 6288305  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin F.  
; APPLICANT: Ferrandiz, Cristina  
; TITLE OF INVENTION: Seed Plants Characterized by Delayed  
; TITLE OF INVENTION: Seed Dispersal  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/349,677  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/067,800  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UD 2948  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 896 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 7..753  
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; NAME/KEY: misc\_feature  
; LOCATION: 896  
; OTHER INFORMATION: /note= "There is a poly(A) tail at  
; OTHER INFORMATION: the end of the cDNA sequence."  
; FEATURE:  
; NAME/KEY: misc\_feature  
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; OTHER INFORMATION: /note= "AGL1 cDNA and deduced  
; OTHER INFORMATION: protein sequences."  
US-09-349-677-5

Query Match 56.0%; Score 536.8; DB 4; Length 896;  
Best Local Similarity 82.1%; Pred. No. 4.6e-175;  
Matches 632; Conservative 0; Mismatches 132; Indels 6; Gaps 1;

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Qy 497 GAACCTTGAAGTAGGCTTGAGAAAGGAATCAGTCGTGTCGGATCCCAAGAGCAGAGAT 556  
Db 426 AAACCTAGAAGGAGCGTCTTGAAGAAAGGAATCAGCCGTGTCGGTCCCAAGAAAGATGAGCT 485  
Qy 557 GTTAGTTGAGAGATTGAATACATGCAAAAAGGAAATCGAGCTGCAAAACGATAACAT 616  
Db 486 GTTAGTGGCAGAGATAGATATATGCAAGAGAGGGAATGGAGTTGCAACACAATAACAT 545  
Qy 617 GTATCTCCGCTCCAAAGTACTGAA-----AGAACAGGTCTTACAGCAACAAGATCGAG 670  
Db 546 GTACCTCGGACCAAGATAGCCGAGGCGCAGATTGAATCCGAGCCAGCAGGAATCGAG 605  
Qy 671 TGTGATACATCAAGGACAGTTTACGAGTCGGGTGTTACTTCTTCTCACCAGTCGGGGCA 730  
Db 606 TGTGATACAAAGGACAGAGTTTACGAATCCGGTGATCTTCTCATGACGAGTCGACGCA 665  
Qy 731 GTATAACCGGAATTATATTCGGTTAACTTCTTGAACCGAATCAGAAATTCCTCCAACCA 790  
Db 666 TTATAATCGGAACATATATTCGGTGAACCTTCTTGAACCGAATCAGCAATTCCTCGGCGCA 725  
Qy 791 AGACCAACCACTCTGCAACTTGTGATTGATTCAGTCTTAACATAAGCTTCCT 840  
Db 726 AGACCAACCTCTCTTCAACTTGTGTAACCTCAAAACATGATAACTTGTTT 775

RESULT 5  
US-09-067-800-4  
; Sequence 4, Application US/09067800  
; Patent No. 6198024  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin F.  
; APPLICANT: Ferrandiz, Cristina  
; TITLE OF INVENTION: Seed Plants Characterized by Delayed  
; TITLE OF INVENTION: Seed Dispersal  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/067,800  
FILING DATE:

## CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UD 2948

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 6138 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 1..6138

OTHER INFORMATION: /label= AGL5\_promoter

OTHER INFORMATION: /note= "Nucleotide sequence of the AGL5 promoter."

US-09-067-800-4

Query Match 34.3%; Score 329; DB 4; Length 6138;  
Best Local Similarity 100.0%; Pred. No. 8.6e-103;  
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 631 AGATTACTGAAAGAACAGGCTCTACAGCAACAAGAAATCGAGTGTGATACATCAAGGGACAG 690

Db 5733 AGATTACTGAAAGAACAGGCTCTACAGCAACAAGAAATCGAGTGTGATACATCAAGGGACAG 5792

QY 691 TTTACGAGTCGGGTGTACTTCTTCTCACCAGTCGGGCGCAGTATAACCGGAATTATATTG 750

Db 5793 TTTACGAGTCGGGTGTACTTCTTCTCACCAGTCGGGCGCAGTATAACCGGAATTATATTG 5852

QY 751 CGGTTAACCTTTTGAACCGAATCAGAAATTCCTCCAAACCAAGACCACCTCTGCAAC 810

Db 5853 CGGTTAACCTTTTGAACCGAATCAGAAATTCCTCCAAACCAAGACCACCTCTGCAAC 5912

QY 811 TTGTTTGAATTCAGTCTAACATAGCTTCTTCTCAGCTGAGATCGATCTATAGTGTC 870

Db 5913 TTGTTTGAATTCAGTCTAACATAGCTTCTTCTCAGCTGAGATCGATCTATAGTGTC 5972

QY 871 CCTAAATGCGGCGCGCTCCCTCAACATCTAGTCGCAAGCTGAGGGGAACCACTAGTGTC 930

Db 5973 CCTAAATGCGGCGCGCTCCCTCAACATCTAGTCGCAAGCTGAGGGGAACCACTAGTGTC 6032

QY 931 TACGAACCTCCAAGAGACGGTTACACAAA 959

Db 6033 TACGAACCTCCAAGAGACGGTTACACAAA 6061

RESULT 6

US-09-349-677-4

; Sequence 4, Application US/09349677

; Patent No. 6288305

; GENERAL INFORMATION:

; APPLICANT: Yanofsky, Martin F.

; APPLICANT: Ferrandiz, Cristina

; TITLE OF INVENTION: Seed Plants Characterized by Delayed

; TITLE OF INVENTION: Seed Dispersal

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESS: Campbell & Flores LLP

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: United States

; ZIP: 92122

; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/349,677  
FILING DATE:

## CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/067,800

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UD 2948

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 6138 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 1..6138

OTHER INFORMATION: /label= AGL5\_promoter

OTHER INFORMATION: /note= "Nucleotide sequence of the AGL5 promoter."

US-09-349-677-4

Query Match 34.3%; Score 329; DB 4; Length 6138;  
Best Local Similarity 100.0%; Pred. No. 8.6e-103;  
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 631 AGATTACTGAAAGAACAGGCTCTACAGCAACAAGAAATCGAGTGTGATACATCAAGGGACAG 690

Db 5733 AGATTACTGAAAGAACAGGCTCTACAGCAACAAGAAATCGAGTGTGATACATCAAGGGACAG 5792

QY 691 TTTACGAGTCGGGTGTACTTCTTCTCACCAGTCGGGCGCAGTATAACCGGAATTATATTG 750

Db 5793 TTTACGAGTCGGGTGTACTTCTTCTCACCAGTCGGGCGCAGTATAACCGGAATTATATTG 5852

QY 751 CGGTTAACCTTTTGAACCGAATCAGAAATTCCTCCAAACCAAGACCACCTCTGCAAC 810

Db 5853 CGGTTAACCTTTTGAACCGAATCAGAAATTCCTCCAAACCAAGACCACCTCTGCAAC 5912

QY 811 TTGTTTGAATTCAGTCTAACATAGCTTCTTCTCAGCTGAGATCGATCTATAGTGTC 870

Db 5913 TTGTTTGAATTCAGTCTAACATAGCTTCTTCTCAGCTGAGATCGATCTATAGTGTC 5972

QY 871 CCTAAATGCGGCGCGCTCCCTCAACATCTAGTCGCAAGCTGAGGGGAACCACTAGTGTC 930

Db 5973 CCTAAATGCGGCGCGCTCCCTCAACATCTAGTCGCAAGCTGAGGGGAACCACTAGTGTC 6032

QY 931 TACGAACCTCCAAGAGACGGTTACACAAA 959

Db 6033 TACGAACCTCCAAGAGACGGTTACACAAA 6061

RESULT 7

US-08-460-512-6

; Sequence 6, Application US/08460512

; Patent No. 5744693

; GENERAL INFORMATION:

; APPLICANT: MEYEROWITZ, Elliot M.

; APPLICANT: YANOFKY, Martin F.

; APPLICANT: MA, Hong

; TITLE OF INVENTION: PLANTS HAVING ALTERED FLORAL DEVELOPMENT

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Richard F. Trecartin

; STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/460,512  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/293,278  
FILING DATE:  
APPLICATION NUMBER: US/07/956,694  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-57322/RFT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1125 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 110..853  
US-08-460-512-6

Query Match 33.2%; Score 318.4; DB 1; Length 1125;  
Best Local Similarity 65.8%; Pred. No. 1.3e-99;  
Matches 479; Conservative 0; Mismatches 246; Indels 3; Gaps 1;

Qy 117 AAGAAGATAGGAGGAGGAAGATAGAGATAAAGAGGATAGAGAACACTAGCAATCGTCAA 176  
Db 152 AGGAACCTGGGAGAGGAAGATAGATCAACCGGATCGAAGAACACAAAGATCGTCAA 211  
Qy 177 GTCACCTTCTGCAACACGCAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGCTTG 236  
Db 212 GTCACCTTCTGCAAGAGACGCAATGGTTTACTCAAAAGGCTTATGAATATCTGCTC 271  
Qy 237 TGTGACCTGAGGTGCTTGTCTTCTCCACTCGAGGCCGCTCTACGAGTACGCC 296  
Db 272 TGTGATGCTGAGGTGCTTGTGTTCTCAAGCAGAGGCGAGACTCTATGAGTATGCC 331  
Qy 297 AACAAAGTGTGAGAGGAACAATAGAAAGGTACAAAGAGCTTGTCCGAGCCCGTTAAC 356  
Db 332 AACAAAGTGTGAAAGCAACAATGAGAGGTACAAAGAGCTTGTTCAGATTCCTCAAC 391  
Qy 357 CTTCCGACCATCACCAAGCTAATACTCAGTACTATCAGCAAGAGCGGTCTFAAATCCGG 416  
Db 392 ACTGGTTCAATTTCCGAGGCCAATGCTCAGTATATCAGCAAGAGCCTTCAAACTGCC 451  
Qy 417 AGCAGATTCCGGACATTCAGAAATTTGAACAGACACATCTTGGTGAATCTTGGTTCC 476  
Db 452 GCACAAATTTGGAATCTGCAGAAATTCAGAAAGGAAACATGTTGGGTGAATCACTGGCTGCA 511  
Qy 477 TTGAACCTTAAGAACTCAAGAACCTTGAAGTAGGTTTGAAAGAAATCAGTCTGTC 536  
Db 512 CTGAGCCTCAGAGATCTGAAGAATCTGGAACAAAATTTGAAAAGGCATTAGCAAAATC 571  
Qy 537 CGATCCAAAGACGACGAGATGTTAGTTGTCAGAGATTGAATACATGCAAAAAGGGAATC 596  
Db 572 AGATCCAAAAGAAATGAGCTGCTGTTGCTGAATTCAGTACATGCAGAGAGGGAAT 631

Qy 597 GAGCTGCAAAACGATAACATGTATCTCCGCTCCAAAGATTACTGAAA---GAACAGGTCTA 653  
Db 632 GATTTACAAACAACAATCAGTACCTGAGAGCAAAAGATTGCTGAAACTGAGAGAGCTCAG 691  
Qy 654 CAGCAACAAGAATCGAGTGTATACATCAAGGGACAGTTTACAGTCCGGGTGTACTTCT 713  
Db 692 CAGCAGCAGCAGCAGCAGCAGTGAATGATGCCAGGAGTCAAGCTATGAGCTTGTG 751  
Qy 714 TCTCACCAGTCGGGGCAGTATAACCGGAATTATATTGGGTTAACCTTCTTGAACCGAAT 773  
Db 752 CCTCCACCTCATCAATTTGATACTCGAAACTATTACAAAGTTAATGGTTGCAAAACCAAC 811  
Qy 774 CAGAAATCTCTCCAAACAGACACCAACCACTCTGCAACTTGTTCAGTCTTAACATAA 833  
Db 812 AACCATTACACTAGACAAGACCAACCACTCTCTTCAACTAGTCTAATATGGTTGAAAGTCT 871  
Qy 834 GCTTCTTT 841  
Db 872 TCTATGTT 879

RESULT 8

US-09-410-464-15  
; Sequence 15, Application US/09410464  
; Patent No. 6395892  
; GENERAL INFORMATION:  
; APPLICANT: Strauss et al.  
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in  
; TITLE OF INVENTION: poplar and other plant species.  
; FILE REFERENCE: 53375  
; CURRENT APPLICATION NUMBER: US/09/410,464  
; CURRENT FILING DATE: 1999-10-01  
; EARLIER APPLICATION NUMBER: 09/287,700  
; EARLIER FILING DATE: 1999-04-06  
; EARLIER APPLICATION NUMBER: 60/080,851  
; EARLIER FILING DATE: 1998-04-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 714  
; TYPE: DNA  
; ORGANISM: Populus balsamifera subsp. trichocarpa  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(714)  
US-09-410-464-15

Query Match 30.0%; Score 287.6; DB 4; Length 714;  
Best Local Similarity 71.7%; Pred. No. 4.1e-89;  
Matches 377; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

Qy 117 AAGAAGATAGGAGGAGGAAGATAGAGATAAAGAGGATAGAGAACACTAGCAATCGTCAA 176  
Db 40 AGGAACCTGGGAGGGAAGGTGGAGATCAAGCGATCGAGAACACCAACCAATCGCCAA 99  
Qy 177 GTCACCTTCTGCAACGACGCAATGGTTTACTCAAGAAAGCTTATGAGCTCTGTCTTG 236  
Db 100 GTCACCTTCTGCAAAAGCGGAATGGTTTGTCAAGAAAGCCTATGAATATCTCTTCT 159  
Qy 237 TGTGACCTGAGGTGCTCTTGTCTATCTTCCACTCGAGGCCGCTCTACGAGTACGCC 296  
Db 160 TCCGATGCTGAGGTGCTATCTGCTCTTCTCCAGCGCTGACAGATTCCTTCCAAC 219  
Qy 297 AACACAGTGTGAGAGAACAAATAGAAAGTTACAAAGAGCTTGTCCGAGCCGCTTAAC 356  
Db 220 AACATAGTGTCAATCTACAATTTGAAAGGTACAAAAGGATGTCAGATTCCTTCCAAC 279  
Qy 357 CTTCCGACCATCACCAAGCTAATACTCAGTACTATCAGCAAGAGCGGTCTAAACTCCGG 416  
Db 280 AACGGTTCAGTTTCTGAAGCCCAATGCTCAGTCTTCTATCAGCAAGAGCTGCCAAGTCCG 339  
Qy 417 AGACAGATTCGGGACATTCAGAATTTGAACAGACACATCTTGGTGAATCTCTTGGTTCC 476





Db 520 GACTTGCAACAATAACCAGCTTCTCCGAGCAAAAGATTTCAGAGA 565

RESULT 11

US-09-410-464-10

; Sequence 10, Application US/09410464

; Patent No. 6395892

; GENERAL INFORMATION:

; APPLICANT: Strauss et al.

; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in

; TITLE OF INVENTION: poplar and other plant species.

; FILE REFERENCE: 53375

; CURRENT APPLICATION NUMBER: US/09/410,464

; CURRENT FILING DATE: 1999-10-01

; EARLIER APPLICATION NUMBER: 09/287,700

; EARLIER FILING DATE: 1999-04-06

; EARLIER APPLICATION NUMBER: 60/080,851

; EARLIER FILING DATE: 1998-04-06

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 10

; LENGTH: 1219

; TYPE: DNA

; ORGANISM: Populus balsamifera subsp. trichocarpa

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (196)..(921)

US-09-410-464-10

Query Match 29.7%; Score 284.4; DB 4; Length 1219;

Best Local Similarity 71.3%; Pred. No. 7.4e-88;

Matches 375; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

QY 117 AAGAGATAGGAGAGGGAAGATAGAGATAAGAGGATAGAGAAACACTACGTAAC 176

Db 235 AGGAAGCTGGGAAGGGGAAGGTGAGATCAAGCGATCGAGAAACACCCACCAATCGCCAA 294

QY 177 GTCACHTTCTGCAACAGCAGCAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGCTTTG 236

Db 295 GTCACHTTCTGCAAGAGGCGAGTGGTTGCTCAAGAAAGCCCTACGAATTATCTGTTCTT 354

QY 237 TGTAGCGTGAAGTGTCTCTGTCATCTTCTCCATCGAGCGCGTCTCTACGAGTACGCC 296

Db 355 TCGATGCTGAGGTGTCACATCGTCTTCTACCGCGCGTCTTATGAGTACTCT 414

QY 297 AACACAGTGTGAGAGGAACAATAAGAGGTACAGAAAGCTTGTCTCCGACGCCGTTAAC 356

Db 415 AACGATAGTGTCAAAATCAACAATTGAGAGGTACAAAAGGCATCTGCAGATTCTTCAAC 474

QY 357 CCTCCGACCATCACCGAAGCTTAATCTCAGTACTATCAGCAAGAGCGTCTAAACTCCGG 416

Db 475 ACTGGGTCTGTTTCTGAAGCCAAATGCTCAGTACTACCAAGAAAGCTGCCAAGCTGCGT 534

QY 417 AGACAGATTCCGGACATTCAGAAATTTGAACAGACACATCTTGGTGAATCTCTTGGTTCC 476

Db 535 TCCCAAAATTTGTAATTTGCAGAAATTCAAACAGGCATATGCTGGGTGAAGCGCTTAGTTCA 594

QY 477 TTGAATTTAAGGAACCTCAAGAACCTTGAAGTAGTGGCTTGAGAAAGGAATCAGTCTGTC 536

Db 595 TTGAGTGTGAAGAACTTAAGAGTTTGGAAATACGACTTGAGAAAGGAATTAAGCAGAAAT 654

QY 537 CGATCCAAAGAACGACGAGATGTTAGTTGACAGATTTGAATACATGCAAAAAGGGAATC 596

Db 655 CTTTCCAAAAGAAATGAGCTGTTGTTGCAAAATCGAGTATATCGAGAGAGGGAGGTT 714

QY 597 GAGCTGCAAAACGATACATGATCTCTCCGCTCCCAAGATTACTGAAA 642

Db 715 GACTTGCAACAATAACAGCTTCTCTCCGAGCAAAAGATTTCAGAGA 760

RESULT 12

US-09-433-579-1

; Sequence 1, Application US/094333579

Db 520 GACTTGCAACAATAACCAGCTTCTCCGAGCAAAAGATTTCAGAGA 565

GENERAL INFORMATION:

APPLICANT: Rottmann, William H.

TITLE OF INVENTION: LSAG Gene

FILE REFERENCE: LSAG Gene

CURRENT APPLICATION NUMBER: US/09/433,579

CURRENT FILING DATE: 1999-11-04

NUMBER OF SEQ ID NOS: 36

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 1297

TYPE: DNA

ORGANISM: Liquidambar styraciflua

FEATURE:

NAME/KEY: CDS

LOCATION: (331)..(1008)

US-09-433-579-1

Query Match 29.3%; Score 280.6; DB 4; Length 1297;

Best Local Similarity 69.8%; Pred. No. 1.16e-86;

Matches 379; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

QY 120 AAGATAGGAGAGGGAAGATAGAGATAAGAGGATAGAGAAACACTACGAATCGTCAAGTC 179

Db 328 AAAATGGTAGGGGAAAGATCGAGATCAAGCGATCGAGAAACACGACAAACCCCAAGTC 387

QY 180 ACTTTCTGCAACAGCAGCAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGCTTGTGT 239

Db 388 ACCTTCTGTAACGGCGCAACGGCTTACTCAAGAAAGCCCTATGAATTTATCTGTTCTGT 447

QY 240 GACGCTGAGGTGCTTCTGTCATCTTCTCCACTCGAGCGCGTCTCTACGAGTACGCCAAC 299

Db 448 GATCCGAGGTAGCCCTTATCGTCTTCTACCGTGGCGCCCTTTAGAGTATGCCAAC 507

QY 300 AACAGTGTGAGAGGAAACAATAAGAGGTACAGAAAGCTTGTCTCCGACGCCGTTAACCT 359

Db 508 AACAGTGTAAAGCAACAATTGAGAGGTATAAGAAAGCACTGTGGATTCCTCCAATACT 567

QY 360 CCGACCATCACCGAAGCTAATCTCAGTACTATCAGCAAGAGCGGTCTAAACTCCGGAGA 419

Db 568 GGATCTGTTTCTGAAGCCAAATGCTCAGTCTTACCAGCAAGAGCTGGCAAACTGCGTAAC 627

QY 420 CAGATTCGGACATTCAGAAATTTGAACAGACACATTTCTGGTGAATCTCTTGGTTCCTTG 479

Db 628 CAAATCAGGAATATCGAGAAATACAAACAGGACTATGCTGGTGAGTCTTTGGGCTCTCTG 687

QY 480 AACTTTAAGGAACCTCAAGAACCTTGAAGTAGGCTTGAGAAAGGAATCAGTCTGTCGGA 539

Db 688 AGTCCCAAGAACTCAAGGCTCTGGAGACTAAATAGAGAAAGGCATTAGCAAAATAAGG 747

QY 540 TCCAAGAGCAGCAGATGTTAGTTGACAGAGATTGAATACATGCAAAAAGGGAATCGAG 599

Db 748 TCCAAAAGAAATGAGCTACTGTTTCCGAAATGAATACATGCAAAAAGGGAATCGAC 807

QY 600 CTGCAAAACGATAACATGATCTCCGCTCCCAAGATTACTGAAAGAACAGGCTCTACAGCAA 659

Db 808 TTGCACAATGATAACAGTATCTCCGAGCAAAAATAGTGAACACGAGAGAGCTCAACAG 867

QY 660 CAA 662

Db 868 CAA 870

RESULT 13

US-08-460-512-3

; Sequence 3, Application US/08460512

; Patent No. 5744693

; GENERAL INFORMATION:

; APPLICANT: MEYEROWITZ, Elliot M.

; APPLICANT: YANOFSKY, Martin F.

; APPLICANT: MA, Hong

; TITLE OF INVENTION: PLANTS HAVING ALTERED FLORAL DEVELOPMENT

; NUMBER OF SEQUENCES: 7



;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Richard F. Trecartin  
;; STREET: 4 Embarcadero Center, Suite 3400  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94111  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/460,512  
;; FILING DATE:  
;; CLASSIFICATION: 800  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/293,278  
;; FILING DATE:  
;; APPLICATION NUMBER: US/07/956,694  
;;  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Trecartin, Richard F.  
;; REGISTRATION NUMBER: 31,801  
;; REFERENCE/DOCKET NUMBER: A-57322/RFT  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 781-1989  
;; TELEFAX: (415) 398-3249  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1097 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: cDNA  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 126..884  
;;  
US-08-460-512-3

Query Match 29.2%; Score 279.6; DB 1; Length 1097;  
Best Local Similarity 70.7%; Pred. No. 3.1e-86;  
Matches 372; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

QY 117 AAGAAGATAGGAGAGGAGGAGATAGAGATAAAGAGGATAGAGAACACTACGAAATCGTCAA 176  
Db 168 AGGAAGCTGGGAGAGGAGGAGATCGAATAAAGCGGATCGAGAACACACGACCGTCAA 227  
QY 177 GTCACTTTCTGCAAAACGACGCAATGTTTACTCAAGAAAGCTTATGAGCTCTGTCTTG 236  
Db 228 GTTACTTTCTGCAAAACGACGCAATGTTTACTCAAGAAAGCTTATGAGCTCTGTCTTG 287  
QY 237 TGTGACGCTGAGGTTGCTTCTTCTCATCTTCTCCACTCGAGGCGCTCTCTACGAGTACGCC 296  
Db 288 TGTGATGCTGAAGTCGCACTCATCTTCTTCTTAGCGGTCGCGCTCTCTATGAGTACTCA 347  
QY 297 AACACAGTGTGAGAGAACAAATAGAAAGGTACAAGAAAGCTTGTCTCCGACGCCGTTAAAC 356  
Db 348 AACACAGTGTGAGAGAACAAATAGAAAGGTACAAGAAAGCTTGTCTCCGACGCCGTTAAAC 407  
QY 357 CCTCCGACCATCACCAGGCTAAATACTCAGTACTATCAGCAAGAGGCGCTTAAACTCCGG 416  
Db 408 ACCGGATCCGTCGCAAGAAATTAATGCACAGTATTAATCAACAGAAATCTGCCAAATTCGCT 467  
QY 417 AGACAGATTCGGGACATTCAGAAATTTCAACACAGACACATCTTGGTGAATCTCTTGGTTCC 476  
Db 468 CAACAAATTTATCAGCATACAGAACTCGAACAGGCAATTAATGCACAGTATTAATCAACAGAAATTCGCT 527  
QY 477 TTGAACCTTTAAGGAACCTCAAGAACCTTGAAGTAGGCTTGAGAAAGGAATCAAGTCTGTC 536  
Db 528 ATGTCCTCCAAAGAGCTCAGGAACCTTGGGAGGAGGAGTATGAGAGAGTGTTAATCGAATC 587  
QY 537 CGATCCAAGAGACGACGAGATCTTAGTTGCAGAGATTGAATACATGCAAAAAAGGGAAATC 596

Db 588 CGATCCAAGAAAGGAACTCTTATTCGCCGAATTTGACTATGATCGAAGAGAGAGT 647  
QY 597 GAGCTGCAAAACGATACATGATCTCGGCTCCAGATTACTGAAA 642  
Db 648 GATTGCATACGATAAACGAGCTTCTTCGTGCTAAGATAGCTGAAA 693  
RESULT 14  
US-08-460-512-1  
; Sequence 1, Application US/08460512  
; Patent No. 5744693  
; GENERAL INFORMATION:  
; APPLICANT: MEYEROWITZ, Elliot M.  
; APPLICANT: YANOFKY, Martin F.  
; APPLICANT: MA, Hong  
; TITLE OF INVENTION: PLANTS HAVING ALTERED FLORAL DEVELOPMENT  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Richard F. Trecartin  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/460,512  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/293,278  
; FILING DATE:  
; APPLICATION NUMBER: US/07/956,694  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Trecartin, Richard F.  
; REGISTRATION NUMBER: 31,801  
; REFERENCE/DOCKET NUMBER: A-57322/RFT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1457 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 416..1270  
; US-08-460-512-1

Query Match 28.5%; Score 273.2; DB 1; Length 1457;  
Best Local Similarity 70.0%; Pred. No. 6.1e-84;  
Matches 368; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

QY 117 AAGAAGATAGGAGAGGAGGAGATAGAGATAAAGAGATAGAGAACACTACGAAATCGTCAA 176  
Db 557 AGGAATCTGGGAGAGGAGGAGATCGAATAAAGCGGATCGAGAACACACGAAATCGTCAA 616  
QY 177 GTCACTTTCTGCAAAACGACGCAATGTTTACTCAAGAAAGCTTATGAGCTCTGTCTTG 236  
Db 617 GTCACTTTTGCAGAAAGTAAATGTTTCTCAAGAAAGCTTATGAGCTCTGTCTTC 676  
QY 237 TGTGACGCTGAGGTTGCTTGTGTCATCTTCTCCACTCGAGGCGCTCTCTACGAGTACGCC 296  
Db 677 TGTGATGCTGAAGTCGCACTCATCTTCTTAGCCGTGGTCTCTATGAGTACTCT 736



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 2, 2003, 05:45:28 ; Search time 237.294 Seconds  
(without alignments)  
9101.213 Million cell updates/sec

Title: US-09-978-382A-5  
Perfect score: 959  
Sequence: 1 gaattcatcttccatctc.....ccaagagacggttacacaa 959

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_101002:\*  
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22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*  
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*  
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 959   | 100.0       | 959    | AAV99860 | Arabidopsis AGL5 c |
| 2          | 735   | 76.6        | 777    | AAC43464 | Arabidopsis thalia |
| 3          | 538   | 56.1        | 1202   | AAC34634 | Arabidopsis thalia |
| 4          | 536.8 | 56.0        | 896    | AAV99859 | Arabidopsis AGL1 c |
| 5          | 475.4 | 49.6        | 511    | AAC33755 | Arabidopsis thalia |
| 6          | 465   | 48.5        | 511    | AAC45357 | Arabidopsis thalia |
| 7          | 329   | 34.3        | 6138   | AAV99858 | Arabidopsis AGL5 g |
| 8          | 329   | 34.3        | 6138   | AAH77275 | Arabidopsis dehisc |
| 9          | 305.8 | 31.9        | 1143   | AAT34428 | Eucalyptus AGE1 cD |

|    |       |      |      |    |          |                    |
|----|-------|------|------|----|----------|--------------------|
| 10 | 287.6 | 30.0 | 714  | 22 | AAF85402 | Nucleotide sequenc |
| 11 | 287.6 | 30.0 | 1115 | 21 | AAZ57949 | Poplar floral home |
| 12 | 287.6 | 30.0 | 1159 | 22 | AAF85401 | Nucleotide sequenc |
| 13 | 287.6 | 30.0 | 1159 | 24 | ABK88491 | Poplar floral home |
| 14 | 285.4 | 29.8 | 1157 | 21 | AAZ50201 | Petunia hybrida ne |
| 15 | 285.4 | 29.8 | 1157 | 21 | AAZ35494 | Petunia nectary-sp |
| 16 | 284.4 | 29.7 | 723  | 22 | AAF85399 | Nucleotide sequenc |
| 17 | 284.4 | 29.7 | 1201 | 21 | AAZ57947 | Poplar floral home |
| 18 | 284.4 | 29.7 | 1219 | 22 | AAF85398 | Nucleotide sequenc |
| 19 | 284.4 | 29.7 | 1219 | 24 | ABK88489 | Poplar floral home |
| 20 | 273.2 | 28.5 | 903  | 21 | AAC51039 | Arabidopsis thalia |
| 21 | 270   | 28.2 | 1053 | 21 | AAC46362 | Arabidopsis thalia |
| 22 | 270   | 28.2 | 1057 | 17 | AAC37453 | Arabidopsis thalia |
| 23 | 268.8 | 28.0 | 997  | 17 | AAT34432 | Arabidopsis thalia |
| 24 | 264.8 | 27.6 | 706  | 21 | AAC55965 | Eucalyptus AGE2 cd |
| 25 | 255.6 | 26.7 | 909  | 21 | AAAG9364 | Eucalyptus grandis |
| 26 | 252.6 | 26.3 | 1218 | 21 | AAC43678 | Plant PrAG1 promot |
| 27 | 252   | 26.3 | 805  | 24 | ABK82084 | Zea mays DNA fragm |
| 28 | 252   | 26.3 | 1259 | 24 | ABK82131 | DNA encoding novel |
| 29 | 242.6 | 25.3 | 1321 | 21 | AAC47718 | DNA encoding novel |
| 30 | 219   | 22.8 | 581  | 21 | AAC57270 | Zea mays DNA fragm |
| 31 | 188   | 19.6 | 466  | 21 | AAC35890 | Eucalyptus grandis |
| 32 | 188   | 19.6 | 5622 | 20 | AAV99857 | Zea mays DNA fragm |
| 33 | 188   | 19.6 | 5622 | 24 | AAH77274 | Arabidopsis AGL1 g |
| 34 | 186.2 | 19.4 | 845  | 24 | ABN98876 | Arabidopsis dehisc |
| 35 | 161.6 | 16.9 | 457  | 21 | AAC41474 | Arabidopsis thalia |
| 36 | 159.2 | 16.6 | 352  | 21 | AAC55878 | Zea mays DNA fragm |
| 37 | 159   | 16.6 | 1144 | 19 | AAV18014 | Eucalyptus grandis |
| 38 | 156.4 | 16.3 | 423  | 21 | AAC56741 | Pinus radiata cone |
| 39 | 152.6 | 15.9 | 1075 | 21 | AAC46463 | Eucalyptus grandis |
| 40 | 150.4 | 15.7 | 498  | 20 | AAV69758 | Arabidopsis thalia |
| 41 | 148.4 | 15.5 | 1062 | 20 | AAX18594 | Tobacco ovary-spec |
| 42 | 148.4 | 15.5 | 1062 | 20 | AAV99856 | Arabidopsis AGL8 n |
| 43 | 147.6 | 15.4 | 1044 | 20 | AAV71739 | Arabidopsis AGL8-1 |
| 44 | 147.6 | 15.4 | 1044 | 21 | AAL44853 | Rice OSMADS6 cDNA. |
| 45 | 146.8 | 15.3 | 1123 | 21 | AAC41877 | Plant flowering ti |
|    |       |      |      |    |          | Arabidopsis thalia |

## ALIGNMENTS

## RESULT 1

AAV99860  
ID AAV99860 standard; cDNA; 959 BP.

AC AAV99860;

XX 10-MAY-1999 (first entry)

DE Arabidopsis AGL5 cDNA.

KW AGL5-like gene; agamous-like 5 gene; seed dispersal; dehiscence;  
KW transgenic plant; promoter; ss.

XX Arabidopsis thaliana.

OS Arabidopsis thaliana.  
FH Key Location/Qualifiers  
FT CDS 78..818  
FT /\*tag= a

XX WO9900502-A1.  
XX 07-JAN-1999.

XX 25-JUN-1998; 98WO-US13208.

XX 28-APR-1998; 98US-0067800.

PR 27-JUN-1997; 97US-0051030.

XX (REGC ) UNIV CALIFORNIA.

PA Ferrandiz C, Yanofsky MF;

XX



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|----|--------------|---------------|----|--------------|---------------|
| PR | 19-MAY-1999; | 99US-0134941. | PR | 28-JUL-1999; | 99US-0145951. |
| PR | 20-MAY-1999; | 99US-0135124. | PR | 02-AUG-1999; | 99US-0146386. |
| PR | 21-MAY-1999; | 99US-0135353. | PR | 02-AUG-1999; | 99US-0146388. |
| PR | 24-MAY-1999; | 99US-0135629. | PR | 02-AUG-1999; | 99US-0146389. |
| PR | 25-MAY-1999; | 99US-0136021. | PR | 03-AUG-1999; | 99US-0147038. |
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| PR | 28-MAY-1999; | 99US-0136782. | PR | 04-AUG-1999; | 99US-0147302. |
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| PR | 10-JUN-1999; | 99US-0138540. | PR | 09-AUG-1999; | 99US-0147935. |
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| Matches 735; Conservative |     | 0; Mismatches 0; Indels 0; Gaps 0;                             |               |
| Qy                        | 78  | ATGGAGGGTGGTGCAGTAATGAAGTACGAGAGCAGCAGCAAGAGATAGGGAGGGAAG      | 137           |
| Db                        | 1   | ATGGAGGGTGGTGCAGTAATGAAGTACGAGAGCAGCAGCAAGAGATAGGGAGGGAAG      | 60            |
| Qy                        | 138 | ATAGAGATAAAGAGGATAGAGAACAACACTACGAATCGTCAAGTCACTTTCTGCAACGACGC | 197           |
| Db                        | 61  | ATAGAGATAAAGAGGATAGAGAACAACACTACGAATCGTCAAGTCACTTTCTGCAACGACGC | 120           |
| Qy                        | 198 | AATGGTTTACTCAAGAAAGCTTATCAGCTCTCTGTGCTGTGTGACGCTGAGGTGCTCTT    | 257           |
| Db                        | 121 | AATGGTTTACTCAAGAAAGCTTATCAGCTCTCTGTGCTGTGTGACGCTGAGGTGCTCTT    | 180           |
| Qy                        | 258 | GTCATCTTCTCCACTCGAGCGCTCTCTACGAGTACGCCCAACAACAGTGTGAGAGGAACA   | 317           |
| Db                        | 181 | GTCATCTTCTCCACTCGAGCGCTCTCTACGAGTACGCCCAACAACAGTGTGAGAGGAACA   | 240           |
| Qy                        | 318 | ATAGAAAGGTACAAGAAAGCTTGTCGCGCCGCTTAACCCCTCCGACCAATCACCGAAGCT   | 377           |
| Db                        | 241 | ATAGAAAGGTACAAGAAAGCTTGTCGCGCCGCTTAACCCCTCCGACCAATCACCGAAGCT   | 300           |
| Qy                        | 378 | AATACTCAGTACTATCAGCAAGAGGCGCTCTAAACCTCCGGAGACAGATTCGGACATTCAG  | 437           |
| Db                        | 301 | AATACTCAGTACTATCAGCAAGAGGCGCTCTAAACCTCCGGAGACAGATTCGGACATTCAG  | 360           |
| Qy                        | 438 | AATTTGAACACACACATCTTGGTGAATCTCTTGGTTCCTTGAACCTTTAAGGAACCTCAAG  | 497           |
| Db                        | 361 | AATTTGAACACACACATCTTGGTGAATCTCTTGGTTCCTTGAACCTTTAAGGAACCTCAAG  | 420           |
| Qy                        | 498 | AACCTTGAAGTAGGCTTGAGAAAGGAATCAGTCGTGTCGATCCAAAGACACAGATG       | 557           |
| Db                        | 421 | AACCTTGAAGTAGGCTTGAGAAAGGAATCAGTCGTGTCGATCCAAAGACACAGATG       | 480           |
| Qy                        | 558 | TTAGTTCAGAGATTGAATACATGCAAAAAGGGGAATCGAGCTGCAAAACGATTAACATG    | 617           |
| Db                        | 481 | TTAGTTCAGAGATTGAATACATGCAAAAAGGGGAATCGAGCTGCAAAACGATTAACATG    | 540           |
| Qy                        | 618 | TATCTCGCTCCAAGATTACTGAAAGAACAGGTCTACAGCAACAAGAAATCGAGTGTGATA   | 677           |
| Db                        | 541 | TATCTCGCTCCAAGATTACTGAAAGAACAGGTCTACAGCAACAAGAAATCGAGTGTGATA   | 600           |
| Qy                        | 678 | CATCAAGGGACAGTTTACGAGTCGGGTGTTACTTCTCTCACCAGTCGGGCGAGTATAAC    | 737           |
| Db                        | 601 | CATCAAGGGACAGTTTACGAGTCGGGTGTTACTTCTCTCACCAGTCGGGCGAGTATAAC    | 660           |
| Qy                        | 738 | CGGAATTATATTGGCGTTAACCCTTCTGAAACCGAATCAGAAATTCCTCCAACCAAGACCAA | 797           |
| Db                        | 661 | CGGAATTATATTGGCGTTAACCCTTCTGAAACCGAATCAGAAATTCCTCCAACCAAGACCAA | 720           |
| Qy                        | 798 | CCACCTCTGCAACTT 812                                            |               |
| Db                        | 721 | CCACCTCTGCAACTT 735                                            |               |

RESULT 3  
AAC34634  
ID AAC34634 standard; DNA: 1202 BP.  
XX AC  
XX AAC34634;  
XX AC  
DT 17-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 7334.

XX Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
XX  
OS Arabidopsis thaliana.  
XX  
EP1033405-A2.  
PN  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-0301439.  
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PR 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 23-APR-1999; 99US-0130891.  
PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
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PR 07-MAY-1999; 99US-0132863.  
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PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
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PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.





|          |                                                                  |                                                                |      |
|----------|------------------------------------------------------------------|----------------------------------------------------------------|------|
| Db       | 561                                                              | AATTGAAAGGTACAAGAAAGCTTTGTCGGATCGCGTCAACCCCTCTCCGTCAACGAAGC    | 620  |
| Qy       | 377                                                              | TAATACTCAGTACTATCAGCAAGAGCGGCTTAATACTCCGAGACAGATTCGGACATTC     | 436  |
| Db       | 621                                                              | TAATACTCAGTACTATCAGCAAGAGCGCTTAAGCTTCGGAGCAGATTCGATATTC        | 680  |
| Qy       | 437                                                              | GAATTGTAACAGACACATCTTGGTGAATCTCTTGGTTCCTTGAACCTTTAAGAACTCAA    | 496  |
| Db       | 681                                                              | GAATTCAAATAGGCATATTTGGGGAATCACTTGGTTCCTTGAACCTTCAAGAACTCAA     | 740  |
| Qy       | 497                                                              | GAACCTTGAAGTAGGCTTCAGAAAGGAATCAGTCGTGTCGGATCCCAAGAACGAGAT      | 556  |
| Db       | 741                                                              | AAACCTAGAAGGACGCTCTTGAAAAAGGAATCAGCCGTGTCGGCTCCAAAAAGAAATGAGCT | 800  |
| Qy       | 557                                                              | GTTAGTTCAGAGATTGAATACATGCAAAAAAGGAAATCGAGCTGCAAAACGATAACAT     | 616  |
| Db       | 801                                                              | GTTAGTTCAGAGATAGATATATGCAAGAGGGAATGGAGTTGCAACACAATAACAT        | 860  |
| Qy       | 617                                                              | GTATCTCCGCTCCAAGATTACTGAA-----AGAACACGGTCTACAGCAACAAAGAAATCGAG | 670  |
| Db       | 861                                                              | GTACCTGCGAGCAAGATACCCGAAGGCGCCAGATTGAATCCGGACCAAGCAATCGAG      | 920  |
| Qy       | 671                                                              | TGTGATACATCAAGGACAGCTTTACGAGTCGGGTGTTACTTCTTCTCACCAGTCGGGCA    | 730  |
| Db       | 921                                                              | TGTGATACAAAGGACGACAGCTTTACGAATCCCGGTGTATCTTCTATGACCAAGTCGCA    | 980  |
| Qy       | 731                                                              | GTATACCGGAAATATATTCGGGTTAACTCTTTGAACCGAAATCAGAATTCCTCCCAACCA   | 790  |
| Db       | 981                                                              | TTATAATCGGAATATATTCGGGTGAACCTTCTTGAACCGAAATCAGCAATTCCTCCGGCCA  | 1040 |
| Qy       | 791                                                              | AGACCAACCACTCTGCAACTTGTGTTGATTGATTCAGTCTAAGCTTCTT 840          |      |
| Db       | 1041                                                             | AGACCAACCTCCTCTCAACTTGTGTTAATCAAAACATGATAACTTGT 1090           |      |
| RESULT 4 |                                                                  |                                                                |      |
| ID       | AAV99859 standard; cdNA; 896 BP.                                 |                                                                |      |
| XX       | AAV99859;                                                        |                                                                |      |
| AC       | AAV99859;                                                        |                                                                |      |
| XX       | 10-MAY-1999 (first entry)                                        |                                                                |      |
| XX       | Arabidopsis AGL1 cDNA.                                           |                                                                |      |
| XX       | AGL1-like gene; agamous-like 1 gene; seed dispersal; dehiscence; |                                                                |      |
| KW       | transgenic plant; promoter; ss.                                  |                                                                |      |
| XX       | Arabidopsis thaliana.                                            |                                                                |      |
| XX       | Key Location/Qualifiers                                          |                                                                |      |
| PH       | CDS 7..753                                                       |                                                                |      |
| FT       | /*tag= a                                                         |                                                                |      |
| FT       | 896                                                              |                                                                |      |
| FT       | polyA_site /*tag= b                                              |                                                                |      |
| XX       | WO9900502-A1.                                                    |                                                                |      |
| PN       | 07-JAN-1999.                                                     |                                                                |      |
| PD       | 25-JUN-1998; 98WO-US13208.                                       |                                                                |      |
| XX       | 28-APR-1998; 98US-0067800.                                       |                                                                |      |
| PR       | 27-JUN-1997; 97US-0051030.                                       |                                                                |      |
| XX       | (REGC ) UNIV CALIFORNIA.                                         |                                                                |      |
| PA       | Ferrandiz C, Yanofsky MF;                                        |                                                                |      |
| XX       | WPI; 1999-095747/08.                                             |                                                                |      |
| PI       | P-PSDB; AAW80999.                                                |                                                                |      |
| XX       |                                                                  |                                                                |      |

|    |                                                                      |                                                               |     |
|----|----------------------------------------------------------------------|---------------------------------------------------------------|-----|
| PT | Use of agamous-like nucleic acids - useful for the production of     |                                                               |     |
| PT | transgenic seed plants in which dehiscence is modified resulting in  |                                                               |     |
| PT | delayed seed dispersal                                               |                                                               |     |
| XX | Disclosure; Page 87-88; 126pp; English.                              |                                                               |     |
| PS | This is the nucleotide sequence of an Arabidopsis agamous-like 1     |                                                               |     |
| XX | (AGL1) gene cDNA clone that codes for AGL1 polypeptide (see          |                                                               |     |
| CC | AAW80999) which is involved in the regulation of dehiscence. The     |                                                               |     |
| CC | invention provides a transgenic seed plant, such as an agl1 and      |                                                               |     |
| CC | agl5 double mutant, that is characterised by delayed seed dispersal  |                                                               |     |
| CC | due to suppression of AGL1 and AGL5 (see AAV99860) expression. The   |                                                               |     |
| CC | invention also provides dehiscence zone regulatory elements, derived |                                                               |     |
| CC | from the AGL1 or AGL5 gene (see AAV99857 and AAV99858), that confer  |                                                               |     |
| CC | selective expression upon an operatively linked nucleic acid         |                                                               |     |
| CC | molecule in the valve margin or dehiscence zone of a seed plant.     |                                                               |     |
| CC | The transgenic seed plants include members of the Brassicaceae,      |                                                               |     |
| CC | such as rapeseed, and members of the Fabaceae, such as soybean,      |                                                               |     |
| CC | pea, lentil and bean. A plant expression vector comprising a         |                                                               |     |
| CC | dehiscence zone-selective regulatory element, and a kit for          |                                                               |     |
| CC | producing the transgenic seed plants are also provided.              |                                                               |     |
| XX | Sequence 896 BP; 285 A; 186 C; 205 G; 220 T; 0 other;                |                                                               |     |
| SQ | Query Match 56.0%; Score 536.8; DB 20; Length 896;                   |                                                               |     |
|    | Best Local Similarity 82.1%; Pred. No. 5.7e-156;                     |                                                               |     |
|    | Matches 632; Conservative 0; Mismatches 132; Indels 6; Gaps 1;       |                                                               |     |
| QY | 77                                                                   | AATGGAGGTGGTCCGAGTAATGAGTAGCAGAGACGACGAAGATAGGGAGAGGAA        | 136 |
| Db | 6                                                                    | AATGGAGGAAGGTGGGAGTAGTCAGCAGCAGAGAGTAGCAAGAACTAGGGAGAGGAA     | 65  |
| QY | 137                                                                  | GATAGAGATAAAGAGGATAGAGAACACTACGATCGTCAAGTCACCTTTCTGCAACGAGC   | 196 |
| Db | 66                                                                   | AATAGAGATAAAGAGGATAGAGAACACAACTCGTCAAGTTACTTTCTGCAACGAGC      | 125 |
| QY | 197                                                                  | CAATGGTCTTACTCAAGAAAGCTTATAGCTCTCTGTCTTGTGTGACGGTGGCTCT       | 256 |
| Db | 126                                                                  | CAATGGTCTTCTCAAGAAAGCTTATGACTCTCTGTCTGTGTGATGCCGAAGTTGCCCT    | 185 |
| QY | 257                                                                  | TGTCATCTTCTCCACTCGAGGCCGTCTCTACGAGTACGCCAACACAGTGTGAGAGGAAC   | 316 |
| Db | 186                                                                  | CGTCATCTTCTCCACTCGTGGCCGTCTCTATGATAGTACGCCAACACAGTGTGAGGGGTAC | 245 |
| QY | 317                                                                  | AATAGAAAGGTACAGAAAGCTTGTCTCCGACGCCGTTAACCCCTCCGACCATCACCGAAGC | 376 |
| Db | 246                                                                  | AATTCGAAAGGTACAGAAAGCTTGTTCGATGCCGTCAACCCCTCTTCGGTCAACCGAAGC  | 305 |
| QY | 377                                                                  | TAATACTCAGTACTATCAGCAAGAGCGGTCTAACTCCGGAGACAGATTCGGGACATTC    | 436 |
| Db | 306                                                                  | TAATACTCAGTACTATCAGCAAGAGCCCTTAAGCTTCGGAGGCAGATTCGAGATATTC    | 365 |
| QY | 437                                                                  | GAATTTGAACAGACACATTTCTTGGTGAATCTCTTGGTTCCTTGAACCTTTAAGGAAC    | 496 |
| Db | 366                                                                  | GAATTCAAATAGGCATATTTGTTGGGAATCCTTGGTTCCTTGAACCTTCAAGGAAC      | 425 |
| QY | 497                                                                  | GAACCTTGAAGTAGGCTTGAGAAAGGAATCAGTCGTGTCCGATCCCAAGAACGACGAG    | 556 |
| Db | 426                                                                  | AAACCTAGAAGGACGCTCTTGAAAAGGAATCAGCGGTGTCGGCTCCAAAGAAATGAGCT   | 485 |
| QY | 557                                                                  | GTTAGTTGCAGAGATTGAATACATGCAAAAAAGGAAATCGAGCTGCAAAACGATAACAT   | 616 |
| Db | 486                                                                  | GTTAGTGGCAGAGATAGATATATCAGAAAGAGGGAATGGAGTTGCAACACAATAACAT    | 545 |
| QY | 617                                                                  | GTATCTCCGCTCCAAGATTACTGAA-----AGAACAGGTCTACAGCAACAAAGAAATCGAG | 670 |
| Db | 546                                                                  | GTACCTGCGAGCAAGATAGCCGAAGGCGCCAGATTGAATCCGGACCAAGCAAGAAATCGAG | 605 |
| QY | 671                                                                  | TGTGATACATCAAGGACAGTTTACGAGTCGGGTGTTACTTCTTCTCACCAGTCGGGGCA   | 730 |
| Db | 606                                                                  | TGTGATACAGGGACAGACATTTACGAATCCGGTGTATCTTCTCATGACCAGTCGAGCA    | 665 |
| QY | 731                                                                  | GTATAACCGGAATTATATTCGGGTTAACTTCTTGAACCGAATCAGAAATTCCTCCAAACCA | 790 |

|          |                                                                |                                                              |     |
|----------|----------------------------------------------------------------|--------------------------------------------------------------|-----|
| Db       | 666                                                            | TTATAATCGGAACATATATTCGGTGAACCTTCTTGAACCGAATCAGCAATTCTCCGGCCA | 725 |
| QY       | 791                                                            | AGACCAACCACTCTGCAACTTGTGATTTCAGTCTAACATAAGCTTCTT             | 840 |
| Db       | 726                                                            | AGACCAACCTCTTCAACTTGTGTAACCTCAAAACATGATAACTTGTTT             | 775 |
| RESULT 5 |                                                                |                                                              |     |
| ID       | AAC33755 standard; DNA; 511 BP.                                |                                                              |     |
| XX       | AC                                                             | AAC33755;                                                    |     |
| XX       | AC                                                             | AAC33755;                                                    |     |
| DT       | 17-OCT-2000                                                    | (first entry)                                                |     |
| DE       | Arabidopsis thaliana DNA fragment SEQ ID NO: 4200.             |                                                              |     |
| XX       | Arabidopsis thaliana.                                          |                                                              |     |
| KW       | Hybridisation assay; genetic mapping; gene expression control; |                                                              |     |
| KW       | protein identification; signal transduction pathway;           |                                                              |     |
| KW       | metabolic pathway; promoter; termination sequence; ss.         |                                                              |     |
| XX       | Arabidopsis thaliana.                                          |                                                              |     |
| XX       | OS                                                             | Arabidopsis thaliana.                                        |     |
| XX       | XX                                                             | EP1033405-A2.                                                |     |
| PN       | XX                                                             | 06-SEP-2000.                                                 |     |
| PD       | XX                                                             | 25-FEB-2000; 2000EP-0301439.                                 |     |
| PF       | XX                                                             | 25-FEB-1999; 99US-0121825.                                   |     |
| PR       | PR                                                             | 05-MAR-1999; 99US-0123180.                                   |     |
| PR       | PR                                                             | 09-MAR-1999; 99US-0123548.                                   |     |
| PR       | PR                                                             | 23-MAR-1999; 99US-0125788.                                   |     |
| PR       | PR                                                             | 25-MAR-1999; 99US-0126264.                                   |     |
| PR       | PR                                                             | 29-MAR-1999; 99US-0126785.                                   |     |
| PR       | PR                                                             | 01-APR-1999; 99US-0127462.                                   |     |
| PR       | PR                                                             | 06-APR-1999; 99US-0128234.                                   |     |
| PR       | PR                                                             | 16-APR-1999; 99US-0128714.                                   |     |
| PR       | PR                                                             | 19-APR-1999; 99US-0129845.                                   |     |
| PR       | PR                                                             | 21-APR-1999; 99US-0130077.                                   |     |
| PR       | PR                                                             | 23-APR-1999; 99US-0130449.                                   |     |
| PR       | PR                                                             | 23-APR-1999; 99US-0130510.                                   |     |
| PR       | PR                                                             | 28-APR-1999; 99US-0130891.                                   |     |
| PR       | PR                                                             | 30-APR-1999; 99US-0131449.                                   |     |
| PR       | PR                                                             | 04-MAY-1999; 99US-0132048.                                   |     |
| PR       | PR                                                             | 05-MAY-1999; 99US-0132407.                                   |     |
| PR       | PR                                                             | 06-MAY-1999; 99US-0132484.                                   |     |
| PR       | PR                                                             | 06-MAY-1999; 99US-0132485.                                   |     |
| PR       | PR                                                             | 06-MAY-1999; 99US-0132486.                                   |     |
| PR       | PR                                                             | 07-MAY-1999; 99US-0132487.                                   |     |
| PR       | PR                                                             | 11-MAY-1999; 99US-0132863.                                   |     |
| PR       | PR                                                             | 14-MAY-1999; 99US-0134256.                                   |     |
| PR       | PR                                                             | 14-MAY-1999; 99US-0134219.                                   |     |
| PR       | PR                                                             | 14-MAY-1999; 99US-0134221.                                   |     |
| PR       | PR                                                             | 14-MAY-1999; 99US-0134370.                                   |     |
| PR       | PR                                                             | 18-MAY-1999; 99US-0134768.                                   |     |
| PR       | PR                                                             | 19-MAY-1999; 99US-0134941.                                   |     |
| PR       | PR                                                             | 20-MAY-1999; 99US-0135124.                                   |     |
| PR       | PR                                                             | 21-MAY-1999; 99US-0135353.                                   |     |
| PR       | PR                                                             | 24-MAY-1999; 99US-0135629.                                   |     |
| PR       | PR                                                             | 25-MAY-1999; 99US-0136021.                                   |     |
| PR       | PR                                                             | 27-MAY-1999; 99US-0136392.                                   |     |
| PR       | PR                                                             | 28-MAY-1999; 99US-0136782.                                   |     |
| PR       | PR                                                             | 01-JUN-1999; 99US-0137222.                                   |     |
| PR       | PR                                                             | 03-JUN-1999; 99US-0137528.                                   |     |
| PR       | PR                                                             | 04-JUN-1999; 99US-0137502.                                   |     |
| PR       | PR                                                             | 07-JUN-1999; 99US-0137724.                                   |     |
| PR       | PR                                                             | 08-JUN-1999; 99US-0138094.                                   |     |
| PR       | PR                                                             | 10-JUN-1999; 99US-0138540.                                   |     |
| PR       | PR                                                             | 10-JUN-1999; 99US-0138847.                                   |     |
| PR       | PR                                                             | 14-JUN-1999; 99US-0139119.                                   |     |
| PR       | PR                                                             | 16-JUN-1999; 99US-0139452.                                   |     |
| PR       | PR                                                             | 16-JUN-1999; 99US-0139453.                                   |     |
| PR       | PR                                                             | 17-JUN-1999; 99US-0139454.                                   |     |
| PR       | PR                                                             | 18-JUN-1999; 99US-0139455.                                   |     |
| PR       | PR                                                             | 18-JUN-1999; 99US-0139456.                                   |     |
| PR       | PR                                                             | 18-JUN-1999; 99US-0139457.                                   |     |
| PR       | PR                                                             | 18-JUN-1999; 99US-0139458.                                   |     |
| PR       | PR                                                             | 18-JUN-1999; 99US-0139459.                                   |     |
| PR       | PR                                                             | 18-JUN-1999; 99US-0139460.                                   |     |
| PR       | PR                                                             | 18-JUN-1999; 99US-0139461.                                   |     |
| PR       | PR                                                             | 18-JUN-1999; 99US-0139462.                                   |     |
| PR       | PR                                                             | 18-JUN-1999; 99US-0139463.                                   |     |
| PR       | PR                                                             | 18-JUN-1999; 99US-0139750.                                   |     |
| PR       | PR                                                             | 21-JUN-1999; 99US-0139817.                                   |     |
| PR       | PR                                                             | 22-JUN-1999; 99US-0139899.                                   |     |
| PR       | PR                                                             | 23-JUN-1999; 99US-0140353.                                   |     |
| PR       | PR                                                             | 23-JUN-1999; 99US-0140354.                                   |     |
| PR       | PR                                                             | 24-JUN-1999; 99US-0140695.                                   |     |
| PR       | PR                                                             | 28-JUN-1999; 99US-0140823.                                   |     |
| PR       | PR                                                             | 29-JUN-1999; 99US-0140991.                                   |     |
| PR       | PR                                                             | 30-JUN-1999; 99US-0141287.                                   |     |
| PR       | PR                                                             | 01-JUL-1999; 99US-0141842.                                   |     |
| PR       | PR                                                             | 01-JUL-1999; 99US-0142154.                                   |     |
| PR       | PR                                                             | 02-JUL-1999; 99US-0142055.                                   |     |
| PR       | PR                                                             | 06-JUL-1999; 99US-0142390.                                   |     |
| PR       | PR                                                             | 08-JUL-1999; 99US-0142803.                                   |     |
| PR       | PR                                                             | 09-JUL-1999; 99US-0142920.                                   |     |
| PR       | PR                                                             | 12-JUL-1999; 99US-0142977.                                   |     |
| PR       | PR                                                             | 13-JUL-1999; 99US-0143542.                                   |     |
| PR       | PR                                                             | 14-JUL-1999; 99US-0143624.                                   |     |
| PR       | PR                                                             | 15-JUL-1999; 99US-0144005.                                   |     |
| PR       | PR                                                             | 16-JUL-1999; 99US-0144085.                                   |     |
| PR       | PR                                                             | 16-JUL-1999; 99US-0144086.                                   |     |
| PR       |                                                                |                                                              |     |

|                           |              |                                                          |                                                                   |     |                                                                    |     |
|---------------------------|--------------|----------------------------------------------------------|-------------------------------------------------------------------|-----|--------------------------------------------------------------------|-----|
| PR                        | 12-AUG-1999; | 99US-0148341.                                            | QY                                                                | 62  | GCTAGGGCTTATAGAAATGGAGGGTGGTCCGAGTAAATGAAGTAGCAGAGAGAGCAAGAA       | 121 |
| PR                        | 13-AUG-1999; | 99US-0148565.                                            | Db                                                                | 95  |                                                                    | 154 |
| PR                        | 13-AUG-1999; | 99US-0148684.                                            | QY                                                                | 122 | GATAGGGAGAGGAAGATAGAGATAAGAGGATAGAGAACTACGATCGTCAAGTCAC            | 181 |
| PR                        | 16-AUG-1999; | 99US-0149368.                                            | Db                                                                | 155 |                                                                    | 214 |
| PR                        | 17-AUG-1999; | 99US-0149175.                                            | QY                                                                | 182 | TTTCTGCAACGACGCAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGTGTGTGA           | 241 |
| PR                        | 18-AUG-1999; | 99US-0149426.                                            | Db                                                                | 215 |                                                                    | 274 |
| PR                        | 20-AUG-1999; | 99US-0149722.                                            | QY                                                                | 242 | CGCTGAGGTTGCTTTGTTCATCTTCTCCACTCGAGGCGCTCTACGAGTACGCCAACAA         | 301 |
| PR                        | 20-AUG-1999; | 99US-0149929.                                            | Db                                                                | 275 | CGCTGAGGTTGCTTTGTTCATCTTCTCCACTCGAGGCGCTCTACGAGTACGCCAACAA         | 334 |
| PR                        | 23-AUG-1999; | 99US-0149902.                                            | QY                                                                | 302 | CAGTGTGAGAGGAACAATAGAAAGGTACAAGAAAGCTTGTCTCGACGCCGTTAACCCCTCC      | 361 |
| PR                        | 25-AUG-1999; | 99US-0150566.                                            | Db                                                                | 335 | CAGTGTGAGAGGAACAATAGAAAGGTACAAGAAAGCTTGTCTCGACGCCGTTAACCCCTCC      | 394 |
| PR                        | 26-AUG-1999; | 99US-0151065.                                            | QY                                                                | 362 | GACCATCACCGAAGCTAATFACTACTAGTACTATCATCAGCAAGAGGCGTCTAAACTCCGGAGACA | 421 |
| PR                        | 27-AUG-1999; | 99US-0151066.                                            | Db                                                                | 395 | GACTATCACCGAAGCTAATFACTACTAGTACTATCATCAGCAAGAGGCGTCTAAACTCCGGAGACA | 454 |
| PR                        | 27-AUG-1999; | 99US-0151080.                                            | QY                                                                | 422 | GATTCGGGACATTCAGAAATTTGAACAGACACACATTTCTTGGTGAATCTCTTGGTTCCTT      | 478 |
| PR                        | 30-AUG-1999; | 99US-0151303.                                            | Db                                                                | 455 | GATTCGGGACATTCAGAAATTTGAACAGACACACATTTCTTGGTGAATCTCTTGGTTCCTT      | 511 |
| PR                        | 31-AUG-1999; | 99US-0151438.                                            | RESULT 6                                                          |     |                                                                    |     |
| PR                        | 01-SEP-1999; | 99US-0151930.                                            | AAC45357                                                          |     |                                                                    |     |
| PR                        | 07-SEP-1999; | 99US-0152363.                                            | ID AAC45357 standard; DNA; 511 BP.                                |     |                                                                    |     |
| PR                        | 10-SEP-1999; | 99US-0153070.                                            | XX                                                                |     |                                                                    |     |
| PR                        | 13-SEP-1999; | 99US-0153758.                                            | AC AAC45357;                                                      |     |                                                                    |     |
| PR                        | 15-SEP-1999; | 99US-0154039.                                            | XX                                                                |     |                                                                    |     |
| PR                        | 16-SEP-1999; | 99US-0154039.                                            | DT 18-OCT-2000 (first entry)                                      |     |                                                                    |     |
| PR                        | 20-SEP-1999; | 99US-0154779.                                            | XX                                                                |     |                                                                    |     |
| PR                        | 22-SEP-1999; | 99US-0155139.                                            | DE Arabidopsis thaliana DNA fragment SEQ ID NO: 46222.            |     |                                                                    |     |
| PR                        | 23-SEP-1999; | 99US-0155486.                                            | XX                                                                |     |                                                                    |     |
| PR                        | 24-SEP-1999; | 99US-0155659.                                            | KW Hybridisation assay; genetic mapping; gene expression control; |     |                                                                    |     |
| PR                        | 28-SEP-1999; | 99US-0156458.                                            | KW protein identification; signal transduction pathway;           |     |                                                                    |     |
| PR                        | 29-SEP-1999; | 99US-0156596.                                            | XX metabolic pathway; promoter; termination sequence; ss.         |     |                                                                    |     |
| PR                        | 04-OCT-1999; | 99US-0157117.                                            | XX Arabidopsis thaliana.                                          |     |                                                                    |     |
| PR                        | 05-OCT-1999; | 99US-0157753.                                            | OS                                                                |     |                                                                    |     |
| PR                        | 06-OCT-1999; | 99US-0157865.                                            | XX                                                                |     |                                                                    |     |
| PR                        | 07-OCT-1999; | 99US-0158029.                                            | PN EP1033405-A2.                                                  |     |                                                                    |     |
| PR                        | 08-OCT-1999; | 99US-0158232.                                            | XX                                                                |     |                                                                    |     |
| PR                        | 12-OCT-1999; | 99US-0158369.                                            | PD 06-SEP-2000.                                                   |     |                                                                    |     |
| PR                        | 13-OCT-1999; | 99US-0159293.                                            | XX                                                                |     |                                                                    |     |
| PR                        | 13-OCT-1999; | 99US-0159294.                                            | PF 25-FEB-2000; 2000EP-0301439.                                   |     |                                                                    |     |
| PR                        | 13-OCT-1999; | 99US-0159295.                                            | XX                                                                |     |                                                                    |     |
| PR                        | 14-OCT-1999; | 99US-0159329.                                            | PR 25-FEB-1999; 99US-0121825.                                     |     |                                                                    |     |
| PR                        | 14-OCT-1999; | 99US-0159330.                                            | PR 05-MAR-1999; 99US-0123180.                                     |     |                                                                    |     |
| PR                        | 14-OCT-1999; | 99US-0159331.                                            | PR 09-MAR-1999; 99US-0123548.                                     |     |                                                                    |     |
| PR                        | 14-OCT-1999; | 99US-0159637.                                            | PR 23-MAR-1999; 99US-0125788.                                     |     |                                                                    |     |
| PR                        | 14-OCT-1999; | 99US-0159638.                                            | PR 25-MAR-1999; 99US-0126264.                                     |     |                                                                    |     |
| PR                        | 18-OCT-1999; | 99US-0159584.                                            | PR 29-MAR-1999; 99US-0126785.                                     |     |                                                                    |     |
| PR                        | 21-OCT-1999; | 99US-0160741.                                            | PR 01-APR-1999; 99US-0127462.                                     |     |                                                                    |     |
| PR                        | 21-OCT-1999; | 99US-0160767.                                            | PR 06-APR-1999; 99US-0128234.                                     |     |                                                                    |     |
| PR                        | 21-OCT-1999; | 99US-0160768.                                            | PR 08-APR-1999; 99US-0128714.                                     |     |                                                                    |     |
| PR                        | 21-OCT-1999; | 99US-0160770.                                            | PR 16-APR-1999; 99US-0129845.                                     |     |                                                                    |     |
| PR                        | 21-OCT-1999; | 99US-0160814.                                            | PR 19-APR-1999; 99US-0130077.                                     |     |                                                                    |     |
| PR                        | 21-OCT-1999; | 99US-0160815.                                            | PR 21-APR-1999; 99US-0130449.                                     |     |                                                                    |     |
| PR                        | 22-OCT-1999; | 99US-0160980.                                            | PR 23-APR-1999; 99US-0130510.                                     |     |                                                                    |     |
| PR                        | 22-OCT-1999; | 99US-0160981.                                            | PR 28-APR-1999; 99US-0131449.                                     |     |                                                                    |     |
| PR                        | 25-OCT-1999; | 99US-0161404.                                            | PR 30-APR-1999; 99US-0132048.                                     |     |                                                                    |     |
| PR                        | 25-OCT-1999; | 99US-0161405.                                            | PR 04-MAY-1999; 99US-0132484.                                     |     |                                                                    |     |
| PR                        | 25-OCT-1999; | 99US-0161406.                                            | PR 05-MAY-1999; 99US-0132485.                                     |     |                                                                    |     |
| PR                        | 26-OCT-1999; | 99US-0161359.                                            | PR 06-MAY-1999; 99US-0132486.                                     |     |                                                                    |     |
| PR                        | 26-OCT-1999; | 99US-0161360.                                            | PR 06-MAY-1999; 99US-0132487.                                     |     |                                                                    |     |
| PR                        | 26-OCT-1999; | 99US-0161361.                                            | PR 07-MAY-1999; 99US-0132863.                                     |     |                                                                    |     |
| PR                        | 28-OCT-1999; | 99US-0161920.                                            |                                                                   |     |                                                                    |     |
| PR                        | 28-OCT-1999; | 99US-0161992.                                            |                                                                   |     |                                                                    |     |
| PR                        | 28-OCT-1999; | 99US-0161993.                                            |                                                                   |     |                                                                    |     |
| PR                        | 29-OCT-1999; | 99US-0162142.                                            |                                                                   |     |                                                                    |     |
| Query Match               |              |                                                          | 49.6%; Score 475.4; DB 21; Length 511;                            |     |                                                                    |     |
| Best Local Similarity     |              |                                                          | 99.8%; Pred. No. 4.8e-137;                                        |     |                                                                    |     |
| Matches 476; Conservative |              |                                                          | 0; Mismatches 1; Indels 0; Gaps 0;                                |     |                                                                    |     |
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PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
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PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
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PR 10-JUN-1999; 99US-0138540.  
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PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
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PR 08-JUL-1999; 99US-0142803.  
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PR 12-AUG-1999; 99US-0148341.  
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PR 13-AUG-1999; 99US-0148684.  
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PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150366.  
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PR 27-AUG-1999; 99US-0151065.  
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PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
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PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
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PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.  
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PR 14-OCT-1999; 99US-0159638.  
PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160768.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.















QY 477 TTGAACCTTTAAGGAACTCAAGAACCTTGAAGTAGGCTTGAGAAAGGAATCAGTCGTGTC 536  
Db 533 CTGACTGCAAAAGATCTGAAGGCTGGAGACCAAACTTGAGAAAGGAATTAGTAGAATT 592  
QY 537 CGATCCAAAGAACGAGAGATGTTAGTTGCGAGAGATTGAATACATGCAAAAAAGGGAATC 596  
Db 593 AGGTCCAAAAGATGAATCCTCTGTTGCTGAGATTGAGTATATGCGAAAAAGGGAATTT 652  
QY 597 GAGCTGCAAAACGATAACATGTATCTCCGCTCCAAAGATTACTGAAAG 643  
Db 653 GATTGCAACAACAATCAGATGCTTCGGGCAAGATAGCTGAGAG 699

RESULT 15

AAZ35494

ID AAZ35494 standard; cDNA; 1157 BP.

XX AC AAZ35494;

XX DT 11-APR-2000 (first entry)

XX DE Petunia nectary-specific FBPI5 cDNA.

XX KW FBPI4; nectary; nectar; transgenic plant; honey; ds.

XX OS Petunia hybrida.

XX Key Location/Qualifiers  
FH CDS 179..841  
FT /\*tag= a

XX PN EP974667-Al.

XX PD 26-JAN-2000.

XX PF 16-JUL-1998; 98EP-0202375.

XX PR 16-JUL-1998; 98EP-0202375.

XX PA (CPRO-) CPRO-DLO CENT PLANTENVERDEDELINGS REPROD.

XX PI Creemers J, Angenent GC, Kater MM;

XX DR WPI; 2000-108400/10.

XX DR P-PSDB; AAY58648.

XX PT Novel DNA sequences used to produce modified honey, the metabolites of which can be isolated and purified -

XX PS Claim 5; Page 17; 56pp; English.

XX CC The present sequence is that of Petunia hybrida strain W115 FBPI5 cDNA that was identified in nectary gland cDNA by differential expression. The cDNA encodes a 221-amino acid MADS box protein (see AAY58648) that is specifically expressed in the nectaries of petunia. The present invention provides a method for producing recombinant proteins in honey. The honey is manufactured by insects, preferably honeybees, that collect the nectar of transgenic plants. The FBPI5 gene and its promoter can be utilised in expression cassettes for the production of transgenic plants that produce a protein of interest in their nectar.

XX SQ Sequence 1157 BP; 391 A; 203 C; 229 G; 334 T; 0 other;

Query Match 29.8%; Score 285.4; DB 21; Length 1157;  
Best Local Similarity 71.3%; Pred. No. 6.8e-78;  
Matches 376; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

QY 117 AAGAAGATAGGAGGGAAGATAGAGATAAAGAGGATAGAACACTAGCAATCGTCAA 176  
Db 173 AGGAAGATGGGAAGAGGAAGATTTAGAGGATTGAAAATACAACAATCGTCAA 232

QY 177 GTCACTTTCTGCAAAACGACGCAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGCTTG 236  
Db 233 GTCACTTTCTGTAAGAGAGAAATGGTTGCTTAAAGCTTATGAATTTCTGTTCTT 292  
QY 237 TGTGACGCTGAGGTTGCTTTGTCATCTTCTCCACTCGAGCGCTCTACGAGTACGCC 296  
Db 293 TGTGATGCTGAAGTTGCTCTCATCGTTTCTCAAGCGTGGCGGCTCTATGAATATGCT 352  
QY 297 AACAAACAGTGTGAGAGGAACAATAGAAAGGTACAAGAAAGCTTGCTCCGACGCCGTTAAC 356  
Db 353 AACAAACAGTGTGAAGGCAACAATTGATAGATATAGAAAGCATCCTCAGATTCTCCTCAAC 412  
QY 357 CCTCCGACCATCACCGAAGCTAATACTCAGTACTATCAGCAAGAGCGCTCTAAACTCCGG 416  
Db 413 ACTGGATCTACTTCTGAAGCTAACACTCAGTTTATCAACAAGAGCTGCCAAACTCCGA 472  
QY 417 AGACAGATTCGGACATTCAGAAATTTGAACAGACACATCTTGGTGAATCTCTTGGTTCC 476  
Db 473 GTTCAGATTGGTAACCTTACAGAACTCAACACAGGAACATGCTAGCGGAGTCTCTAAGTTCT 532  
QY 477 TTGAACCTTTAAGGAACTCAAGAACCTTGAAGTAGGCTTGAGAAAGGAATCAGTCGTGTC 536  
Db 533 CTGACTGCAAAAGATCTGAAAGGCTGGAGACCAAACTTGAGAAAGGAATTAGTAGAATT 592  
QY 537 CGATCCAAAGAACGACGAGATGTTAGTTGCGAGAGATTGAATACATGCAAAAAAGGGAATC 596  
Db 593 AGGTCCAAAAGGAATGAATCCTCTGTTGCTGAGATTGAGTATATGCGAAAAAGGGAATTT 652  
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Search completed: February 2, 2003, 08:19:19  
Job time : 259.294 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 2, 2003, 08:19:29 ; Search time 2626.26 Seconds  
(without alignments)  
10627.107 Million cell updates/sec

Title: US-09-978-382A-5  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 7: gb\_ph:\*
- 8: gb\_pl:\*
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- 31: em\_htg\_inv:\*
- 32: em\_htg\_other:\*
- 33: em\_htg\_mus:\*
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- 35: em\_htg\_rod:\*
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- 37: em\_htg\_vrt:\*
- 38: em\_sy:\*
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- 40: em\_htgo\_mus:\*
- 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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| 4          | 536.8 | 56.0          | 895    | 8  | ATHAGL1A  | M5550 Arabidopsis    |
| 5          | 536.8 | 56.0          | 896    | 6  | AR138347  | AR138347 Sequence    |
| 6          | 503.2 | 52.5          | 789    | 8  | AY036062  | AY036062 Brassica    |
| 7          | 329   | 34.3          | 6138   | 6  | AR138346  | AR138346 Sequence    |
| 8          | 329   | 34.3          | 6138   | 6  | AX320930  | AX320930 Sequence    |
| 9          | 328.8 | 34.3          | 1065   | 8  | MDO251117 | AJ251117 Malus dom   |
| 10         | 322.8 | 33.7          | 1065   | 8  | AB025643  | AB025643 Rosa rugo   |
| 11         | 318.4 | 33.2          | 1125   | 6  | AR003863  | AR003863 Sequence    |
| 12         | 318.4 | 33.2          | 1125   | 8  | TOBNAG1A  | L23925 Nicotiana t   |
| 13         | 315.4 | 32.9          | 1160   | 8  | AF265562  | AF265562 Vitis vin   |
| 14         | 314.4 | 32.8          | 1214   | 8  | PHPMADS3  | AF265562 Vitis vin   |
| 15         | 307.6 | 32.1          | 1084   | 8  | TOMTAG1A  | L26295 Lycopersico   |
| 16         | 296.4 | 30.9          | 1009   | 8  | AF234617  | AF234617 Phalaenop   |
| 17         | 295.6 | 30.8          | 1080   | 8  | PGORFGAG2 | Z46612 P.ginseng g   |
| 18         | 295   | 30.8          | 956    | 8  | PHFBP6A   | X68675 P.hybrida f   |
| 19         | 293.6 | 30.6          | 1142   | 8  | AF022377  | AF022377 Cucumis s   |
| 20         | 293.6 | 30.6          | 1197   | 8  | AF103903  | AF103903 Liquidamb   |
| 21         | 293.4 | 30.6          | 1224   | 8  | PETFFHP   | L33973 Petunia inf   |
| 22         | 286.8 | 29.9          | 1201   | 8  | GHY9722   | AJ009722 Gerbera h   |
| 23         | 285.4 | 29.8          | 1073   | 8  | S53900    | S53900 ple=plena l   |
| 24         | 285.4 | 29.8          | 1157   | 6  | AX006357  | AX006357 Sequence    |
| 25         | 285.4 | 29.8          | 1158   | 8  | AF035438  | AF035438 Cucumis s   |
| 26         | 285.4 | 29.8          | 1160   | 8  | AF022379  | AF022379 Cucumis s   |
| 27         | 281.2 | 29.3          | 1128   | 8  | DCA271150 | AJ271150 Daucus ca   |
| 28         | 280.6 | 29.3          | 1082   | 8  | AF265554  | AF265554 Cucumis s   |
| 29         | 280   | 29.2          | 1054   | 8  | AB025644  | AB025644 Rosa rugo   |
| 30         | 279.6 | 29.2          | 1097   | 6  | AR003862  | AR003862 Sequence    |
| 31         | 279.6 | 29.2          | 1098   | 8  | BNABAG1X  | M99415 Brassica na   |
| 32         | 276   | 28.8          | 994    | 8  | GHY9723   | AJ009723 Gerbera h   |
| 33         | 275.6 | 28.7          | 1000   | 8  | AF022378  | AF022378 Cucumis s   |
| 34         | 275.2 | 28.7          | 1116   | 8  | RHU43372  | U43372 Rosa hybrid   |
| 35         | 275   | 28.7          | 967    | 8  | CSCUS1    | X97801 C.sativus C   |
| 36         | 274.4 | 28.6          | 1345   | 8  | CSA312773 | AJ312773 Cucumis s   |
| 37         | 274   | 28.6          | 1073   | 8  | AB025646  | AB025646 Rosa rugo   |
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| 39         | 273.2 | 28.5          | 1457   | 6  | AR003861  | AR003861 Sequence    |
| 40         | 273.2 | 28.5          | 1458   | 8  | ATAGAMSG  | X53579 A.thaliana    |
| 41         | 271.6 | 28.3          | 1048   | 8  | AF035439  | AF035439 Cucumis s   |
| 42         | 270.6 | 28.2          | 1061   | 8  | AF099937  | AF099937 Hyacinthu   |
| 43         | 270.4 | 28.2          | 942    | 8  | AF373604  | AF373604 Vitis vin   |
| 44         | 270.2 | 28.2          | 905    | 8  | ATU20182  | U20182 Arabidopsis   |
| 45         | 270   | 28.2          | 763    | 8  | AY083173  | AY083173 Gossypium   |

ALIGNMENTS

|            |                                                     |                                    |        |     |        |                 |
|------------|-----------------------------------------------------|------------------------------------|--------|-----|--------|-----------------|
| RESULT 1   | AR138348                                            | Sequence 7 from patent US 6198024. | 959 bp | DNA | linear | PAT 16-JUN-2001 |
| AR138348   | LOCUS                                               | AR138348                           |        |     |        |                 |
| DEFINITION | Sequence 7 from patent US 6198024.                  |                                    |        |     |        |                 |
| ACCESSION  | AR138348                                            |                                    |        |     |        |                 |
| VERSION    | AR138348.1                                          | GI:14479857                        |        |     |        |                 |
| KEYWORDS   |                                                     |                                    |        |     |        |                 |
| SOURCE     | Unknown.                                            |                                    |        |     |        |                 |
| ORGANISM   | Unknown.                                            |                                    |        |     |        |                 |
| REFERENCE  | 1 (bases 1 to 959)                                  |                                    |        |     |        |                 |
| AUTHORS    | Yanofsky,M.F. and Ferrandiz,C.                      |                                    |        |     |        |                 |
| TITLE      | Seed plants characterized by delayed seed dispersal |                                    |        |     |        |                 |
| JOURNAL    | Patent: US 6198024-A 7 06-MAR-2001;                 |                                    |        |     |        |                 |
| FEATURES   | Location/Qualifiers                                 |                                    |        |     |        |                 |







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Qy 377 TAATACTCAGTACTATCAGCAAGAGCGCTAAACTCCGAGACAGATTCCGGGACATTCA 436  
Db 621 TAATACTCAGTACTATCAGCAAGAGCGCTTAAGTTTCGGAGGAGATTTCGAGATATTCA 680  
Qy 437 GAATTTGAACAGACACATCTTGGTGAATCTCTTGGTTCCTTGAACCTTTAAAGAACTCAA 496  
Db 681 GAATTCAAATAGGCATATTGTTGGGAATCACCTTGGTTCCTTGAACCTTCAAGGAACCTAA 740  
Qy 497 GAACCTTGAAGTAGGCTTGAGAAAGGAATCAGTCGTGTCGGATCCCAAGAGCAGGAGAT 556  
Db 741 AAACCTAGAGGAGCGCTTGAAGAAAGGAATCAGCGGTGTCGGCTCCCAAGAAAGATGAGCT 800  
Qy 557 GTTAGTTGCAGAGATTGAATACATGCAAAAAGGAAATCGAGCTGCAAAACGATAACAT 616  
Db 801 GTTAGTGGCAGATAGATATATGCAGAGAGGGAAATGAGTTGCAACACAATAACAT 860  
Qy 617 GTATCTCCGCTCCCAAGATTACTGAA-----AGAACAGGTCCTACAGCAACAAGAAATCGAG 670  
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Db 921 TGTGATACAAAGGACGACAGTTTACGAATCCGGGTGTATCTCTCATGACCAGTCGCAGCA 980  
Qy 731 GTATAACCGGAATATATTGGCGGTTAAACCTTCTTGAACCAATCAGAATTCCTCAACCA 790  
Db 981 TTATAATCGGAATATATTCCGGTGAACCTTCTTGAACCGAATCAGCAATTCCTCGGCCA 1040  
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Db 1041 AGACCAACCTCTCTCAACTGTGTAACTCAAAACATGATAACTTGTTT 1090

RESULT 4  
LOCUS ATHAGLLA 895 bp mRNA linear PLN 27-APR-1993  
DEFINITION Arabidopsis thaliana transcription factor (AGL1), complete cds.  
ACCESSION M55550  
VERSION M55550.1 GI:166587  
KEYWORDS transcription factor;  
SOURCE Arabidopsis thaliana (strain Landsberg erecta) flower cDNA to mRNA.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
1 (bases 1 to 895)  
Ma,H., Yanofsky,M.F. and Meyerowitz,E.M.  
AGL1-AGL6, an Arabidopsis gene family with similarity to floral  
homeotic and transcription factor genes  
Genes Dev. 5 (3), 484-495 (1991)  
91160981  
1672119  
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/db\_xref="GI:166588"  
/translation="MEEGGSHDAESSKLRGKIEIKRIENTTNRQVTFCKRRNGLL

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BASE COUNT 284 a 186 c 205 g 220 t  
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Query Match 56.0%; Score 536.8; DB 8; Length 895;  
Best Local Similarity 82.1%; Pred. No. 1.6e-145;  
Matches 632; Conservative 0; Mismatches 132; Indels 6; Gaps 1;  
Qy 77 AATGGAGGGTGGTGGAGTAAATGAAGTAGCAGAGAGCAGCAAGAGATAGGGAGAGGGAA 136  
Db 6 AATGGAGGAAGGTGGAGTAGTCACGACGCGAGAGAGTAGCAAGAACTAGGGAGAGGGAA 65  
Qy 137 GATAGAGATAAGAGGATAGAGAACACTAGCAATCGTCAAGTCACTTTCTGCAACGACG 196  
Db 66 AATAGAGATAAGAGGATAGAGAACACAAATCGTCAAGTTACTTTCTGCAACGACG 125  
Qy 197 CAATGGTTTACTCAAGAAAGCTTATGAGCTCTGTCTTGTGTGACGGTGAAGTTGCTCT 256  
Db 126 CAATGGTCTTCTCAAGAAAGCTTATGAACCTCTCTCTGTGTGATGCCGAAGTTGCCCT 185  
Qy 257 TGTCACTTCTCCACTCGAGGCGGTCTCTACGAGTACGCCAACACACAGTGTGAGAGGAAC 316  
Db 186 CGTCACTTCTCCACTCGTGGCCGCTCTATGAGTACGCCAACACACAGTGTGAGGGGTAC 245  
Qy 317 AATAGAAAGGTACAGAAAGCTTGTCCGACGCCGTAAACCCCTCCGACCATCACCGAAGC 376  
Db 246 AATTGAAAGGTACAGAAAGCTTGTTCGGATCCGCTCAACCCCTCTCCGTCACCGAAGC 305  
Qy 377 TAATACTCAGTACTATCAGCAAGAGCGCTTAAACTCCGAGACAGATTCGGGACATTCA 436  
Db 306 TAATACTCAGTACTATCAGCAAGAGCGCTTAAAGCTTCGAGGCGAGATTCGAGATATTCA 365  
Qy 437 GAATTTGAACAGACACATCTTGGTGAATCTCTTGGTTCCTTGAACCTTTAAGGAACCTCAA 496  
Db 366 GAATTCAAATAGGCATATTGTTGGGAATCACTTGGTTCCTTGAACCTTCAAGGAACCTCAA 425  
Qy 497 GAACCTTGAAGTAGGCTTGAGAAAGGAATCAGTCGTGTCGGATCCCAAGAGCAGGAGAT 556  
Db 426 AAACCTAGAGGAGCGCTTGAAGAAAGGAATCAGCCGTGTCGGCTCCAAAAGAAATGAGCT 485  
Qy 557 GTTAGTTCAGAGATTGAATACATGCAAAAAGGGAATCAGAGCTGCAAAACGATAACAT 616  
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Qy 617 GTATCTCCGCTCCCAAGATTACTGAA-----AGACAGGTCCTACAGCAACAAGAAATCGAG 670  
Db 546 GTACCTCGGAGCAAGATAGCCGAAGGCGCCAGATTGAATCCGGACCGAGGAATTCGAG 605  
Qy 671 TGTGATACATCAAGGACAGATTACGAGTCGGGTGTACTTCTTCTCACCAGTCGGGGCA 730



|                       |                                                     |                                                                 |                                 |
|-----------------------|-----------------------------------------------------|-----------------------------------------------------------------|---------------------------------|
| QY                    | 194                                                 | ACGCAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGTCTTGTGTGAGCTGAGGTTGC     | 253                             |
| Db                    | 156                                                 | ACGCAATGGTCTTCTCAAGAAAGCTTATGAGCTCTCTGTCTTGTGTGAGCTGAGGTTGC     | 215                             |
| QY                    | 254                                                 | TCTTGTCACTTCTCCACCTCGAGGCGCTCTACGAGTAGCGCCAAACAACAGTGTGAGAGG    | 313                             |
| Db                    | 216                                                 | CCTCGTATCTTCTCCACCTCGTGGCTTCTTATGAGTAGCGCCAAACAACAGTGTGAGAGG    | 275                             |
| QY                    | 314                                                 | AACAATAGAAGGTACAAGAAAGCTTGCTCCGAGCGCGTTAACCTCCGACCATCACCGA      | 373                             |
| Db                    | 276                                                 | TACAATAGAAGGTACAAGAAAGCTTGCTCCGAGCGCGTTAACCTCCGACCATCACCGA      | 335                             |
| QY                    | 374                                                 | AGCTAATACCTAGTACTATCAGCAAGAGGCGTCTAAACTCCGGAGACAGATTCGGGACAT    | 433                             |
| Db                    | 336                                                 | AGCTAATACCAAGCACTATCAGCAAGAGGCTCTAAGCTTCGGAGGACAGATTCGGGACAT    | 395                             |
| QY                    | 434                                                 | TCAGAAATTTGAACAGACACATCTTGGTGAATCTCTTGGTTCCTTGAACCTTTAAGGAATC   | 493                             |
| Db                    | 396                                                 | TCAGAAATTTGAACAGGCAATATTTGGGAGAACTACTTGGTTCATTTGAACCTTTAAGGAATC | 455                             |
| QY                    | 494                                                 | CAAGAACCTTGAAAGTAGGCTTGAGAAAGGAATCAGTCGTGTCGGATCCAAAGAACGACGA   | 553                             |
| Db                    | 456                                                 | CAAAACCTTAGAAGGACGCGCTTGAAAAGGAATCAGCCGCTCCGATCCAAAGAGAGTGA     | 515                             |
| QY                    | 554                                                 | GATGTTAGTTCAGAGATTGAATACATGCAAAAAGGGAATTCGAGCTCAAAACGATAA       | 613                             |
| Db                    | 516                                                 | ACTTTAGTGGCAGAGATAGATATATGACAGAGAGGGAATGGAGTTGCAGCACGTTAA       | 575                             |
| QY                    | 614                                                 | CATGATCTCGCTCCAAAGATTACTGAA-----AGAACAGGTCTACAGCAACAAGATTC      | 667                             |
| Db                    | 576                                                 | CATGTAACCTAAGAGCTAAGATAGAACAGCGCGGAGATTGAATCCGGACAGCATGGATC     | 635                             |
| QY                    | 668                                                 | GAGTGTATACATCAAGGGACAGTTTACGAGTCGGGTGTACTTCTTCTC-----ACCAGTC    | 724                             |
| Db                    | 636                                                 | CGGTGTAATACAAAGGACGCGGTTTATGATCGCGTCTCTCTTCTTCTCATGATCAGTC      | 695                             |
| QY                    | 725                                                 | GGGGCAGTATACCGGAATATATATGCGGTAACTTCTTGAACCGAATCAGAAATTCCTC      | 784                             |
| Db                    | 696                                                 | GCAGCATATTAACCGGAATATATATCCGGTTAACCTTCTTGAACCGAATCAACAATTC      | 755                             |
| QY                    | 785                                                 | CAACCAAGACCAACACCTCTGCAACTTGTTGA                                | 818                             |
| Db                    | 756                                                 | CGGTCAAGACCAACCTCTCTCAACTTGTTAA                                 | 789                             |
| RESULT 7              |                                                     |                                                                 |                                 |
| AR138346              |                                                     |                                                                 |                                 |
| LOCUS                 | AR138346                                            | 6138 bp                                                         | DNA linear PAT 16-JUN-2001      |
| DEFINITION            | Sequence 4 from patent US 6198024.                  |                                                                 |                                 |
| ACCESSION             | AR138346                                            |                                                                 |                                 |
| VERSION               | AR138346.1                                          | GI:14479855                                                     |                                 |
| KEYWORDS              | Unknown.                                            |                                                                 |                                 |
| SOURCE                | Unknown.                                            |                                                                 |                                 |
| ORGANISM              | Unclassified.                                       |                                                                 |                                 |
| REFERENCE             | 1 (bases 1 to 6138)                                 |                                                                 |                                 |
| AUTHORS               | Yanofsky,M.F. and Ferrandiz,C.                      |                                                                 |                                 |
| TITLE                 | Seed plants characterized by delayed seed dispersal |                                                                 |                                 |
| JOURNAL               | Patent: US 6198024-A 4 06-MAR-2001;                 |                                                                 |                                 |
| FEATURES              | Location/Qualifiers                                 |                                                                 |                                 |
| source                | 1. .6138                                            |                                                                 |                                 |
| BASE COUNT            | 2002 a 1058 c 931 g 2147 t                          |                                                                 |                                 |
| ORIGIN                | /organism="unknown"                                 |                                                                 |                                 |
| Query Match           | 34.3%;                                              | Score 329;                                                      | DB 6; Length 6138;              |
| Best Local Similarity | 100.0%;                                             | Pred. No. 8.6e-85;                                              |                                 |
| Matches               | 329;                                                | Conservative 0;                                                 | Mismatches 0; Indels 0; Gaps 0; |
| QY                    | 631                                                 | AGATTACTGAAAGAACAGGCTCTACAGCAACAAGAAATCGAGTGTGATACATCAAGGGACAG  | 690                             |
| Db                    | 5733                                                | AGATTACTGAAAGAACAGGCTCTACAGCAACAAGAAATCGAGTGTGATACATCAAGGGACAG  | 5792                            |

|                       |                                                                                                                                                                                               |                                                                |                                 |
|-----------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------|---------------------------------|
| QY                    | 691                                                                                                                                                                                           | TTTACGAGTCGGGTGTTACTTCTTCTCACCAGTCGGGCAGTATAACCGGAATTATATTG    | 750                             |
| Db                    | 5793                                                                                                                                                                                          | TTTACGAGTCGGGTGTTACTTCTTCTCACCAGTCGGGCAGTATAACCGGAATTATATTG    | 5852                            |
| QY                    | 751                                                                                                                                                                                           | CGGTTAACCTTCTTGAACCGAATCAGAAATTCCTCCAAACAAGCAACCACTCTGCAAC     | 810                             |
| Db                    | 5853                                                                                                                                                                                          | CGGTTAACCTTCTTGAACCGAATCAGAAATTCCTCCAAACAAGCAACCACTCTGCAAC     | 5912                            |
| QY                    | 811                                                                                                                                                                                           | TTGTTTGTATTCAGTCTAACATAAGCTTCTTCTCAGCTGAGATCGATCTATAGTGTC      | 870                             |
| Db                    | 5913                                                                                                                                                                                          | TTGTTTGTATTCAGTCTAACATAAGCTTCTTCTCAGCTGAGATCGATCTATAGTGTC      | 5972                            |
| QY                    | 871                                                                                                                                                                                           | CCTAAATGCGGCGCGTCCCTCAACATCTAGTCGCAAGCTGAGGGGAACCACTAGTGTC     | 930                             |
| Db                    | 5973                                                                                                                                                                                          | CCTAAATGCGGCGCGTCCCTCAACATCTAGTCGCAAGCTGAGGGGAACCACTAGTGTC     | 6032                            |
| QY                    | 931                                                                                                                                                                                           | TACGAACCTCCAAGAGACGGTTACACAA                                   | 959                             |
| Db                    | 6033                                                                                                                                                                                          | TACGAACCTCCAAGAGACGGTTACACAA                                   | 6061                            |
| RESULT 8              |                                                                                                                                                                                               |                                                                |                                 |
| AX320930              |                                                                                                                                                                                               |                                                                |                                 |
| LOCUS                 | AX320930                                                                                                                                                                                      | 6138 bp                                                        | DNA linear PAT 14-DEC-2001      |
| DEFINITION            | Sequence 6 from Patent WO0179517.                                                                                                                                                             |                                                                |                                 |
| ACCESSION             | AX320930                                                                                                                                                                                      |                                                                |                                 |
| VERSION               | AX320930.1                                                                                                                                                                                    | GI:17902477                                                    |                                 |
| KEYWORDS              | thale cress.                                                                                                                                                                                  |                                                                |                                 |
| SOURCE                | Arabidopsis thaliana                                                                                                                                                                          |                                                                |                                 |
| ORGANISM              | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. |                                                                |                                 |
| REFERENCE             | 1                                                                                                                                                                                             |                                                                |                                 |
| AUTHORS               | Liljegen,S. and Yanofsky,M.F.                                                                                                                                                                 |                                                                |                                 |
| TITLE                 | Control of fruit dehiscence in arabidopsis by indehiscent1 genes                                                                                                                              |                                                                |                                 |
| JOURNAL               | Patent: WO 0179517-A 6 25-OCT-2001;                                                                                                                                                           |                                                                |                                 |
| FEATURES              | The Regents of the University of California (US)                                                                                                                                              |                                                                |                                 |
| source                | Location/Qualifiers                                                                                                                                                                           |                                                                |                                 |
| 1. .6138              | /organism="Arabidopsis thaliana"                                                                                                                                                              |                                                                |                                 |
| /db_xref="taxon:3702" | /note="SHATTERPROOF2 (SHP2) genomic"                                                                                                                                                          |                                                                |                                 |
| BASE COUNT            | 2002 a 1058 c 931 g 2147 t                                                                                                                                                                    |                                                                |                                 |
| ORIGIN                |                                                                                                                                                                                               |                                                                |                                 |
| Query Match           | 34.3%;                                                                                                                                                                                        | Score 329;                                                     | DB 6; Length 6138;              |
| Best Local Similarity | 100.0%;                                                                                                                                                                                       | Pred. No. 8.6e-85;                                             |                                 |
| Matches               | 329;                                                                                                                                                                                          | Conservative 0;                                                | Mismatches 0; Indels 0; Gaps 0; |
| QY                    | 631                                                                                                                                                                                           | AGATTACTGAAAGAACAGGCTCTACAGCAACAAGAAATCGAGTGTGATACATCAAGGGACAG | 690                             |
| Db                    | 5733                                                                                                                                                                                          | AGATTACTGAAAGAACAGGCTCTACAGCAACAAGAAATCGAGTGTGATACATCAAGGGACAG | 5792                            |
| QY                    | 691                                                                                                                                                                                           | TTTACGAGTCGGGTGTTACTTCTTCTCACCAGTCGGGCAGTATAACCGGAATTATATTG    | 750                             |
| Db                    | 5793                                                                                                                                                                                          | TTTACGAGTCGGGTGTTACTTCTTCTCACCAGTCGGGCAGTATAACCGGAATTATATTG    | 5852                            |
| QY                    | 751                                                                                                                                                                                           | CGGTTAACCTTCTTGAACCGAATCAGAAATTCCTCCAAACAAGCAACCACTCTGCAAC     | 810                             |
| Db                    | 5853                                                                                                                                                                                          | CGGTTAACCTTCTTGAACCGAATCAGAAATTCCTCCAAACAAGCAACCACTCTGCAAC     | 5912                            |
| QY                    | 811                                                                                                                                                                                           | TTGTTTGTATTCAGTCTAACATAAGCTTCTTCTCAGCTGAGATCGATCTATAGTGTC      | 870                             |
| Db                    | 5913                                                                                                                                                                                          | TTGTTTGTATTCAGTCTAACATAAGCTTCTTCTCAGCTGAGATCGATCTATAGTGTC      | 5972                            |
| QY                    | 871                                                                                                                                                                                           | CCTAAATGCGGCGCGTCCCTCAACATCTAGTCGCAAGCTGAGGGGAACCACTAGTGTC     | 930                             |
| Db                    | 5973                                                                                                                                                                                          | CCTAAATGCGGCGCGTCCCTCAACATCTAGTCGCAAGCTGAGGGGAACCACTAGTGTC     | 6032                            |
| QY                    | 931                                                                                                                                                                                           | TACGAACCTCCAAGAGACGGTTACACAA                                   | 959                             |
| Db                    | 6033                                                                                                                                                                                          | TACGAACCTCCAAGAGACGGTTACACAA                                   | 6061                            |

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RESULT 9
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LOCUS      MDO251117      1065 bp      mRNA      linear      PLN 16-NOV-2001
DEFINITION Malus domestica mRNA for C-type MADS box protein (mads14 gene).
ACCESSION AJ251117
VERSION    AJ251117.1 GI:16973295
KEYWORDS   C-type MADS box protein; mads14 gene.
SOURCE     apple tree.
ORGANISM   Malus x domestica
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
REFERENCE 1
AUTHORS    Vosman,B. and Smulders,M.J.M.
TITLE      Isolation of apple B- and C-type MADS box genes from vegetative
            tissue
JOURNAL     Unpublished
            2 (bases 1 to 1065)
AUTHORS     van der Linden,C.G.
TITLE      Direct Submission
JOURNAL     Submitted (15-NOV-1999) van der Linden C.G., Identity and Genetic
            Diversity, CPRO Wageningen University & Research Centre, PO Box 16,
            Wageningen, 6700 AA, NETHERLANDS
FEATURES   Location/Qualifiers
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BASE COUNT 344 a 237 c 211 g 273 t
ORIGIN
Query Match      34.3%; Score 328.8; DB 8; Length 1065;
Best Local Similarity 68.1%; Pred. No. 9.4e-85;
Matches 478; Conservative 0; Mismatches 212; Indels 12; Gaps 1;

QY 117 AAGAAGATAGGAGAGGGAAGATAGAGATAAGAGAGATAGAGAACACTACGAATCGTCAA 176
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 179 AAAAAATTGGGAAGAGGCAAAATTGAGATTAAAGCGGATCGAAACACTACCAATCGACAA 238

QY 177 GTCACATTTCTGCAAAACGACGCAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGTCTTG 236
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 239 GTCACCTTCTGCAACGCGCAACGAGATTGCTTAAGAAAGCCTATGAATTCCTGTCTT 298

QY 237 TGTGACGCTGAGGTTGCTCTGTCTATCTTCTCCACATCGAGCGCCGTCTCTAGAGTAGCGCC 296
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 299 TGTGATGCTGAAGTTGCTCTTCTATCGTCTTCTCCACCGGTGCGCGCTCTATGAGTAGTCT 358

QY 297 AACACAGCTGTAGAGGAACAATAGAAAGGTACAGAAAGCTTGCTCCGACCGGTAAAC 356
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 359 AACACACAGCGTTAGACCAACAATCGACAGGTACAAAAAGCATGCGCTGATCTACGGAC 418

QY 357 CCTCCGACCATCACCGAAGCTAATACCTAGTACTATCAGCAAGAGCGCTCTAAACCTCCGG 416
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 419 GGTGATCTGTATCAGAGCTTAACACTCAGTTTATCAGCAGGAAGCATCAAAACTGCCGA 478

QY 417 AGACAGATTCCGGACATTTCAGAATTGAACAGACACATCTTGGTGAATCTCTTGTTCC 476
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JOURNAL expression of the tobacco floral homeotic gene NAG1  
MEDLINE Plant Physiol. 103 (4), 1041-1046 (1993)  
PUBMED 94120000  
7507255

FEATURES

Location/Qualifiers

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Query Match 33.2%; Score 318.4; DB 8; Length 1125;  
Best Local Similarity 65.8%; Pred. No. 1e-81;  
Matches 479; Conservative 0; Mismatches 246; Indels 3; Gaps 1;

QY 117 AAGAAGTAGGAGGAGGAAGATAGAGATAAGAGGATAGAGAACACTACGAATCGTCAA 176  
DB 152 AGGAACTGGGAGAGGAAAGATAGATCAACCGGATCGAAACACACGAATCGTCAA 211  
QY 177 GTCACCTTCTGCAACACGCGATGGTTTACCAAGAAAGCTTATGAGCTCTCTGTCTG 236  
DB 212 GTCACCTTCTGCAAGAGACGCAATGGTTTACTCAAAAAGCGCTATGAATTAATCTGTGCTC 271  
QY 237 TGTGACGCTGAGTGTCTTGTCTATCTTCTCACTCGAGGCGGTCTCTACGAGTACGCC 296  
DB 272 TGTGATGCTGAGTGTCTTGTATGTTCTCTCAAGCAGGAGGACACCTCTATGAGTATGCC 331  
QY 297 AACAACTGTGAGAGGAGCAATAGAAAGGTACAAAGAGCTTGTCTCGACGCGCTTAAC 356  
DB 332 AACAACTGTGAGAGGAGCAATAGAGAGGTACAAAGAGCTTGTCTCAGATTCCTCAAC 391  
QY 357 CTCCCGACCATCACCGAAGCTAATCTCAGTACTATCAGCAAGAGCGCTTAACTCCGG 416  
DB 392 ACTGGTCAATTTCCGAGGCCAATGCTCAGTATTATCAGCAAGAGCGCTCCAAACTGCGC 451  
QY 417 AGACAGATTCGGGACATTCAGRATTTGAACAGACACATTTCTTGGTGAATCTCTTGGTTC 476  
DB 452 GCACAAATTTGAAATCTGCAGAAATCAGACAGGAACATGTTGGTGAATCACTGGCTGCA 511  
QY 477 TTGAACCTTAAAGAACTCAAGAACCTTGAAGTAGGCTTGAGAAAGGAATCACTCGTGC 536  
DB 512 CTGAGCTCAGAGATCTCAAGATCTGGAACAAAATTTGAAAAGGCATTAGCAAAATC 571  
QY 537 CGATCAAGAAAGCAGAGATGTTAGTGTGAGATTTGAATACATGCAAAAAGGGAAATC 596  
DB 572 AGATCAAAAAGAAATGAGCTGCTGTTGCTGAAATTAGATACATGCAGAGAGGAAAT 631  
QY 597 GAGCTGCAAAACGATTAACATGTATCTCCGCTCCCAAGATTACTGAAA---GAACAGGTCTA 653  
DB 632 GATTTACACAAACAACATCACTACCTGAGAGCAAGATTTGCTGAACTGAGAGAGCTCAG 691  
QY 654 CAGCAACAAGATCGAGTGTGATACATCAAGGGACAGTTTACGAGTGGGTGCTTACTTCT 713  
DB 692 CAGCAGCAGCAGCAGCAGCATGAATTTGATGCCAGGGAGTTCAAGCTATGAGCTGTGTG 751

QY 714 TCTCACCAGTCGGGGCAGTATACCGGAATTTATATTCGGTTAACCTTCTTTGAACCGAAT 773  
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QY 774 CAGAAATCTCCCAACCAAGACCAACACCTCTGCAACTTGTGTGATTCAGTCTAACATAA 833  
DB 812 AACCATACACTAGACAAGACCAACCATCTCTTCAACTAGTCTAATATGTTGAAAGTCT 871  
QY 834 GCTTCTTT 841  
DB 872 TCTATGTT 879

RESULT 13

AF265562 AF265562 1160 bp mRNA linear PLN 09-AUG-2001  
LOCUS Vitis vinifera MAD-box transcription factor (mads1) mRNA, complete  
DEFINITION cds.

ACCESSION AF265562  
VERSION AF265562.1 GI:14279305  
KEYWORDS

SOURCE Vitis vinifera.  
ORGANISM Vitis vinifera

REFERENCE 1 (bases 1 to 1160)  
AUTHORS Boss, P.K., Vivier, M., Matsumoto, S., Dry, I.B. and Thomas, M.R.  
TITLE A cDNA from grapevine (Vitis vinifera L.), which shows homology to  
AGAMOUS and SHATTERPROOF, is not only expressed in flowers but also  
throughout berry development

JOURNAL Plant Mol. Biol. 45 (5), 541-553 (2001)  
MEDLINE 21307190  
PUBMED 11414613  
REFERENCE 2 (bases 1 to 1160)  
AUTHORS Boss, P.K., Vivier, M., Matsumoto, S., Dry, I.B. and Thomas, M.  
TITLE Direct Submission  
JOURNAL Submitted (09-MAY-2000) Plant Industry, CSIRO, Hartley Grove, Glen  
Osmond, SA 5064, Australia

FEATURES  
source  
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BASE COUNT 356 a 241 c 252 g 311 t  
ORIGIN  
Query Match 32.9%; Score 315.4; DB 8; Length 1160;  
Best Local Similarity 67.2%; Pred. No. 7.7e-81;  
Matches 470; Conservative 0; Mismatches 211; Indels 18; Gaps 1;

QY 120 AAGATAGGAGAGGAGGAGATAGAGATAAGAGGATAGAGAACACTACGAATCGTCAAGTC 179  
DB 197 AAATGGGAGAGGAGGAGATCGAAATTAAGCGGATCGAGAACACCCTAATCGCAAGTC 256  
QY 180 ACTTTCTGCAAAACGACGCAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGTCTGTGT 239  
DB 257 ACCTTCTGTAAGCGCGCACGCGCTTGTCTCAAAAAGCGCTATGAATTTATCGGTCTTATGT 316



|            |                                                                                                                                                                                          |                                                                 |                 |
|------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------|-----------------|
| QY         | 240                                                                                                                                                                                      | GACGCTGAGGTTGCTCTTGTTCATCTTCTCCACTCGAGGGCGTCTCTACGAGTACGCCAAC   | 299             |
| Db         | 317                                                                                                                                                                                      | GATCAGAAAGTTGCTCTCATCTCTCCAGCCGTGGCGCCTCTATGAATATGCTAAC         | 376             |
| QY         | 300                                                                                                                                                                                      | AACAGTGTGAGAGGAACAATPAGAAAGGTACAAGAAGCTTGTCTCGACGCCGTTTAAACCC   | 359             |
| Db         | 377                                                                                                                                                                                      | AACAGTGTGAGAACGACAATCGAAAGGTACAAAAGTGTGTTCTGATTCTCTCCRAATACC    | 436             |
| QY         | 360                                                                                                                                                                                      | CCGACCATCCCGAAGCTAATACTCAGTACTATCATCAGCAAGAGGCGCTTAACATCCGGGAGA | 419             |
| Db         | 437                                                                                                                                                                                      | GGATCTGTTTCTGAAGCTAATGCTCAGTCTTACCAGCAAGAGCCCTCCAATTTGCGCGGT    | 496             |
| QY         | 420                                                                                                                                                                                      | CAGATTCGGGACATTCAGAAATTTGAACAGACACATCTTCTGGTGAATCTCTTGGTTCTCTTG | 479             |
| Db         | 497                                                                                                                                                                                      | CAATCAGGCGATATACAGAATTTGAACAGGCATATTCTGGGTGAGGCTCTTAGCTCTCTG    | 556             |
| QY         | 480                                                                                                                                                                                      | AACTTTAAAGAACTCAAGAACCTTTGAAAGTGTGAGAAAGGAATCAGTCGTGTCGA        | 539             |
| Db         | 557                                                                                                                                                                                      | AACTTTAAAGAACTCAAGAACTCTGGAGACAGGCTGGAGAAAGGTATCAGCAGAATCAGA    | 616             |
| QY         | 540                                                                                                                                                                                      | TCCAAAGACGACGAGATGTTAGTTCAGAGATTGAATACATGCAAAAAGGGAATTCGAG      | 599             |
| Db         | 617                                                                                                                                                                                      | TCCAAAAGAAATGAATGCTGTTTGTGTAATCGAGTACATGCAAAAAGGAGAGATTGAG      | 676             |
| QY         | 600                                                                                                                                                                                      | CTGCAAAACGATAACATGTATCTCCGCTCAAGATTACTGAAAGACAGGTCTACAGCAA      | 659             |
| Db         | 677                                                                                                                                                                                      | CTCCAAAACAGTAACTATTCTTCGGAGCACAGATAGCTGAGAATGAGAGAGCCCAACAG     | 736             |
| QY         | 660                                                                                                                                                                                      | CAAGAACTGAGTGTGATACATCAAGGGACAGTTTACGAGTCGGGTGTTACTTCTCTCAC     | 719             |
| Db         | 737                                                                                                                                                                                      | CAATGAACCTGATGCCAGGTCTCAGTACGAGAGCGTGCGG-----                   | 778             |
| QY         | 720                                                                                                                                                                                      | CAGTCGGGGCAGTATAACCCGGAATATATTGCGGTTAACCTTCTTGAACCGAATCAGAAT    | 779             |
| Db         | 779                                                                                                                                                                                      | CAGCAGCCATACGACTCTCAAACTTGCTCCCTGTTAACTCTCTGACCCCTAATCACCAT     | 838             |
| QY         | 780                                                                                                                                                                                      | TCCTCCAACCAAGACCAACACCTCTCGCAACTTGTTTGA                         | 818             |
| Db         | 839                                                                                                                                                                                      | TACTCTCGCCACGACCAACACAGCTCTCCAAGTAGTGTA                         | 877             |
| RESULT 14  |                                                                                                                                                                                          |                                                                 |                 |
| PHPMADS3   |                                                                                                                                                                                          |                                                                 |                 |
| LOCUS      | PHPMADS3                                                                                                                                                                                 | 1214 bp                                                         | mRNA            |
| DEFINITION | P.hybrida pMADS3 mRNA.                                                                                                                                                                   | linear                                                          | PLN 15-NOV-1993 |
| ACCESSION  | X72912                                                                                                                                                                                   |                                                                 |                 |
| VERSION    | X72912.1                                                                                                                                                                                 | GI:313112                                                       |                 |
| KEYWORDS   | homeotic flower gene; MADS box; pMADS3 gene; transcriptional regulation.                                                                                                                 |                                                                 |                 |
| SOURCE     | Petunia x hybrida.                                                                                                                                                                       |                                                                 |                 |
| ORGANISM   | Petunia x hybrida                                                                                                                                                                        |                                                                 |                 |
|            | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Petunia. |                                                                 |                 |
| REFERENCE  | 1 (bases 1 to 1214)                                                                                                                                                                      |                                                                 |                 |
| AUTHORS    | Tsuchimoto,S., van der Krol,A.R. and Chua,N.H.                                                                                                                                           |                                                                 |                 |
| TITLE      | Ectopic expression of pMADS3 in transgenic petunia phenocopies the petunia blind mutant                                                                                                  |                                                                 |                 |
| JOURNAL    | Plant Cell 5 (8), 843-853 (1993)                                                                                                                                                         |                                                                 |                 |
| MEDLINE    | 94004017                                                                                                                                                                                 |                                                                 |                 |
| PUBMED     | 8104573                                                                                                                                                                                  |                                                                 |                 |
| REFERENCE  | 2 (bases 1 to 1214)                                                                                                                                                                      |                                                                 |                 |
| AUTHORS    | Tsuchimoto,S.                                                                                                                                                                            |                                                                 |                 |
| TITLE      | Direct Submission                                                                                                                                                                        |                                                                 |                 |
| JOURNAL    | Submitted (26-MAR-1993) S. Tsuchimoto, The Rockefeller University, 1230 York Ave., New York, NY 10021, USA                                                                               |                                                                 |                 |
| FEATURES   |                                                                                                                                                                                          |                                                                 |                 |
| source     | Location/Qualifiers                                                                                                                                                                      |                                                                 |                 |
|            | 1..1214                                                                                                                                                                                  |                                                                 |                 |
|            | /organism="Petunia x hybrida"                                                                                                                                                            |                                                                 |                 |
|            | /variety="line W115"                                                                                                                                                                     |                                                                 |                 |
|            | /db_xref="taxon:4102"                                                                                                                                                                    |                                                                 |                 |
|            | /sub_clone="pBluescript SK"                                                                                                                                                              |                                                                 |                 |
|            | /tissue_type="all floral tissue"                                                                                                                                                         |                                                                 |                 |

|            |                                                                                                                                                                                                                                                        |                                                                |                                       |
|------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------|---------------------------------------|
| gene       | /clone_lib="lambda ZAP II"                                                                                                                                                                                                                             |                                                                |                                       |
|            | /dev_stage="flower bud"                                                                                                                                                                                                                                |                                                                |                                       |
|            | 159..887                                                                                                                                                                                                                                               |                                                                |                                       |
| CDS        | /gene="pMADS3"                                                                                                                                                                                                                                         |                                                                |                                       |
|            | 159..887                                                                                                                                                                                                                                               |                                                                |                                       |
|            | /gene="pMADS3"                                                                                                                                                                                                                                         |                                                                |                                       |
|            | /note="MADS box-1 subunit"                                                                                                                                                                                                                             |                                                                |                                       |
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| BASE COUNT | 393 a                                                                                                                                                                                                                                                  | 238 c                                                          | 235 g                                 |
| ORIGIN     | 348 t                                                                                                                                                                                                                                                  |                                                                |                                       |
|            | Query Match                                                                                                                                                                                                                                            | 32.8%;                                                         | Score 314.4; DB 8; Length 1214;       |
|            | Best Local Similarity                                                                                                                                                                                                                                  | 66.7%;                                                         | Pred. No. 1.5e-80;                    |
|            | Matches                                                                                                                                                                                                                                                | 472; Conservative                                              | 0; Mismatches 221; Indels 15; Gaps 1; |
| QY         | 117                                                                                                                                                                                                                                                    | AAGAAGATAGGGAGGGAAGATAGAGATAAAGAGGATAGAGAAACACATACGAATCGTCAA   | 176                                   |
| Db         | 201                                                                                                                                                                                                                                                    | AGAAACTAGGAAGAGGAAAGATTGAGATCAAGAGGATCGAAACACGACAAATCGGCAA     | 260                                   |
| QY         | 177                                                                                                                                                                                                                                                    | GTCACTTCTGCAACGACGCAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGTCTTG     | 236                                   |
| Db         | 261                                                                                                                                                                                                                                                    | GTCACTTTTGCAGAGAGACGCAATGGTTTGTCTCAAAAAGCCATTATGATTTATCTGTGCTC | 320                                   |
| QY         | 237                                                                                                                                                                                                                                                    | TGTGACGCTGAGGTTGCTTGTTCATCTTCTCCTCAGTCCGAGGCGCTCTACGAGTACGCC   | 296                                   |
| Db         | 321                                                                                                                                                                                                                                                    | TGTGATGCTGAAGTTGCTTGTGATTGCTCTCTAGCCGAGGCGAGGCTCTATGATGATGCC   | 380                                   |
| QY         | 297                                                                                                                                                                                                                                                    | AACAACAGTGTGAGAGGAACAATPAGAAAGGTACAAGAAGCTTGTCTCGACGCGGTTAAAC  | 356                                   |
| Db         | 381                                                                                                                                                                                                                                                    | AACAACAGTGTGAAAGCACAAATGAGAGGTACAAGAAGCTTGTTCAGATTCTCTCAAC     | 440                                   |
| QY         | 357                                                                                                                                                                                                                                                    | CTCCGACCATCACGAAGCTAATCTCAGTACTATCATCAGCAAGAGCGGCTCTAAACTCCGG  | 416                                   |
| Db         | 441                                                                                                                                                                                                                                                    | ACTGGTTCAATTCGCCGAAGCTAATGCTCAGTATTACCAGCAAGAGCCCTCCAACCTCGT   | 500                                   |
| QY         | 417                                                                                                                                                                                                                                                    | AGACAGATTCGGACATTCAGAAATTTGAACAGACACATCTTCTGCTGAATCTCTTGGTTCC  | 476                                   |
| Db         | 501                                                                                                                                                                                                                                                    | GCACAAATTGAAATCTGCAGAACCAAGAGAACTTTCTTGGTGAATCTCTTGTCTGCA      | 560                                   |
| QY         | 477                                                                                                                                                                                                                                                    | TTGAACTTTAAGAACTCAAGAACCTTGAAAGTAGGCTTGAGAAAGGAATCAGTCGTGTC    | 536                                   |
| Db         | 561                                                                                                                                                                                                                                                    | CTGAATCTCAGAGATCTGAGGAACCTGGACACAAAATTTGAAAAGGCATTAGCAAAATC    | 620                                   |
| QY         | 537                                                                                                                                                                                                                                                    | CGATCCAAAGAACGACGAGATGTTAGTTGCAGAGATTGAATACATGCAGAAAGGGAATC    | 596                                   |
| Db         | 621                                                                                                                                                                                                                                                    | CGAGCCAAAAGAAATGAGCTGTTGCTGAAATTTAGTATATGCAGAAAGAGGAAAT        | 680                                   |
| QY         | 597                                                                                                                                                                                                                                                    | GAGTCGCAAAACGATAACATGTATCTCCGCTCCAAGATTACTGAAAGAACAGGCTCTACAG  | 656                                   |
| Db         | 681                                                                                                                                                                                                                                                    | GATTTACACAAACAATCAGTATTTAGAGCAAGAAATTTGCTGAAACTGAGAGATCCCAG    | 740                                   |
| QY         | 657                                                                                                                                                                                                                                                    | CAACAAGATCGAGTGTGATACATCAAGGACAGTTTACGAGTCGGGTGTTACTTCTTCT     | 716                                   |
| Db         | 741                                                                                                                                                                                                                                                    | CA-----GATGAACCTTGATGCCTGGGAGTTCTAGCTATGACCTTGTGCCT            | 785                                   |
| QY         | 717                                                                                                                                                                                                                                                    | CACAGTCGGGGCAGTATAACCGGAATTAATATTCGGGTTAACCTTCTTGAACCGAATCAG   | 776                                   |
| Db         | 786                                                                                                                                                                                                                                                    | CCCAGCAGTCATTCGATGCGCGGAACATCTACAAGTGAATGGCTTGCAGAGACCAAC      | 845                                   |
| QY         | 777                                                                                                                                                                                                                                                    | AATTCCTCCAACCAAGACCAACCACTCTGCAACTTGTGTGATTCAGT                | 824                                   |
| Db         | 846                                                                                                                                                                                                                                                    | CATTACCCTAGACAAGACCAACCACTCTTCAACTAGTCTAATTTATT                | 893                                   |



RESULT 15

TOMTAG1A 1084 bp mRNA linear PLN 07-JUL-1994  
LOCUS  
DEFINITION Lycopersicon esculentum TAG1 mRNA, complete cds.  
ACCESSION L26295  
VERSION L26295.1 GI:457381  
KEYWORDS  
SOURCE Lycopersicon esculentum (strain VF36) (library: mature tomato pistil cDNA library in lambda gt10 from C. Gasser) mature pistils cDNA to mRNA.

ORGANISM

Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
Lycopersicon.  
1 (bases 1 to 1084)  
Pnuell,L., Hareven,D., Rounsley,S.D., Yanofsky,M.F. and Lifschitz,E.

REFERENCE

AUTHORS

TITLE Isolation of the tomato AGAMOUS gene TAG1 and analysis of its homeotic role in transgenic plants

JOURNAL

Plant Cell 6 (2), 163-173 (1994)

MEDLINE

94198593

PUBMED

7908549

FEATURES

source

CDS

Location/Qualifiers  
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BASE COUNT 378 a 203 c 214 g 289 t  
ORIGIN

Query Match 32.1%; Score 307.6; DB 8; Length 1084;  
Best Local Similarity 65.7%; Pred. No. 1.5e-78;  
Matches 464; Conservative 0; Mismatches 239; Indels 3; Gaps 1;

QY 117 AAGAGATAGGGAGAGGGAGATAGAGATAAGAGAGGATAGAGACACTACGAATCGTCAA 176  
DB 111 AGGAACTAGGAAGGGGAAAATTGAGATCAAAAGGATCGAAACACACGAGATCGACAA 170  
QY 177 GTCACCTTCTGCAACACGCGCAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGCTTG 236  
DB 171 GTACATTCTGCAGAGCGCGCAATGGTTTGTCTTAAAGGCTTATGAATTGCTGTGCTC 230  
QY 237 TGTGACGCTGAGGTTGCTCTGTGCATCTCTCCACTCGAGGCGGCTCTACGAGTACGCC 296  
DB 231 TGTGATGCTGAGGTTGCTTTGGTTGTCTTCTCAACAGAGGCGACACTCTAGTATGCC 290  
QY 297 AACACAGTGTGAGAGGACAAATAGAAAGGTACAAGAAAGCTTGCTCCGACGCCGTTAAC 356  
DB 291 AACACAGTGTGAAAGCAACAATCGAGAGGTACAAGAAAGCATGCTCAGATTCTCCTCAAC 350  
QY 357 CCTCCGACCATCCGAGCTAATFACTAGTACTATCAGCAAGAGCGGCTCTAAACTCCGG 416  
DB 351 ACTGGTTCAGTATCCGAGGCCAATGCTCAGTATTACCAGCAAGAGCCCTCCAACTCGCG 410  
QY 417 AGACAGATTCCGGACATTCAGAAATTGAAACAGACACATCTTGGTGAATCTCTGGTTCC 476

